

Fig.1.

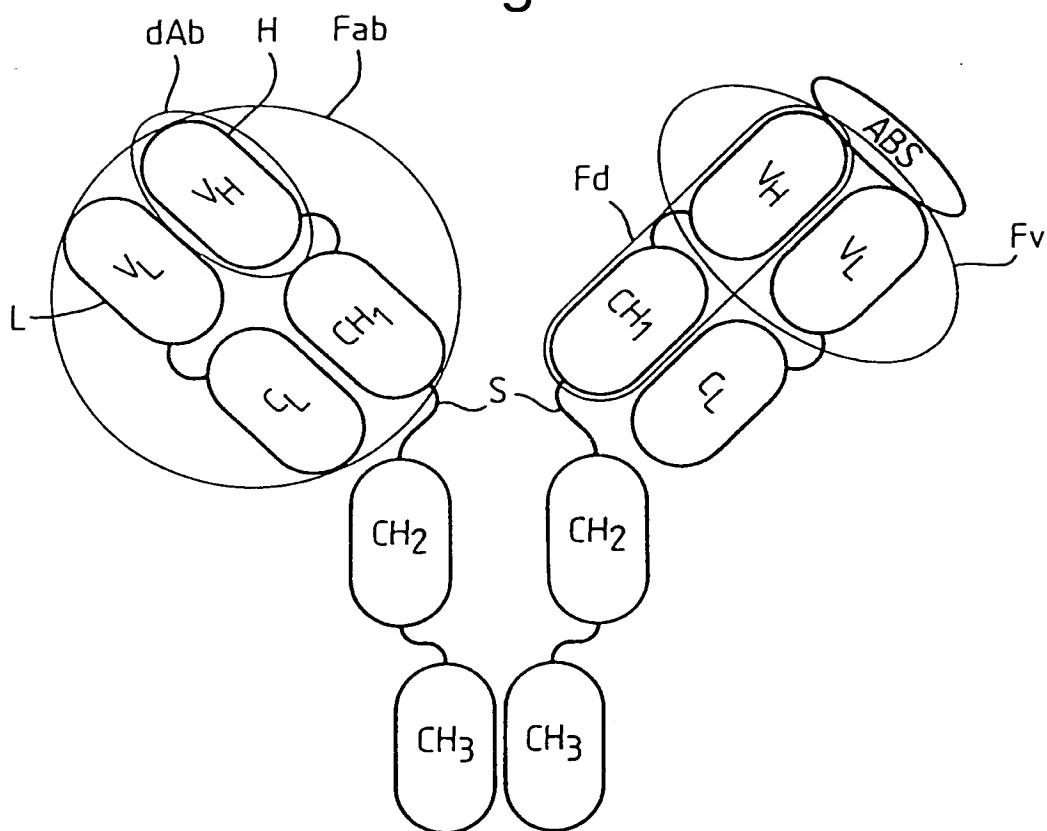


Fig.2a

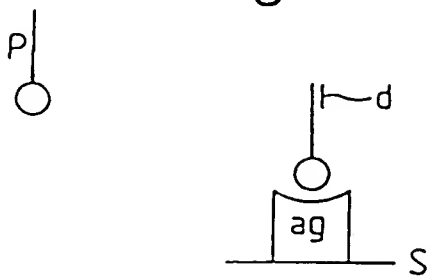


Fig.2b

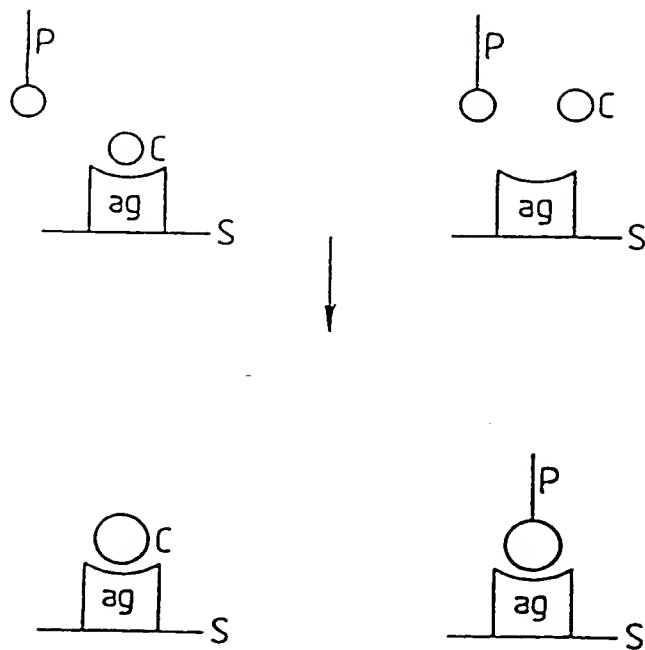
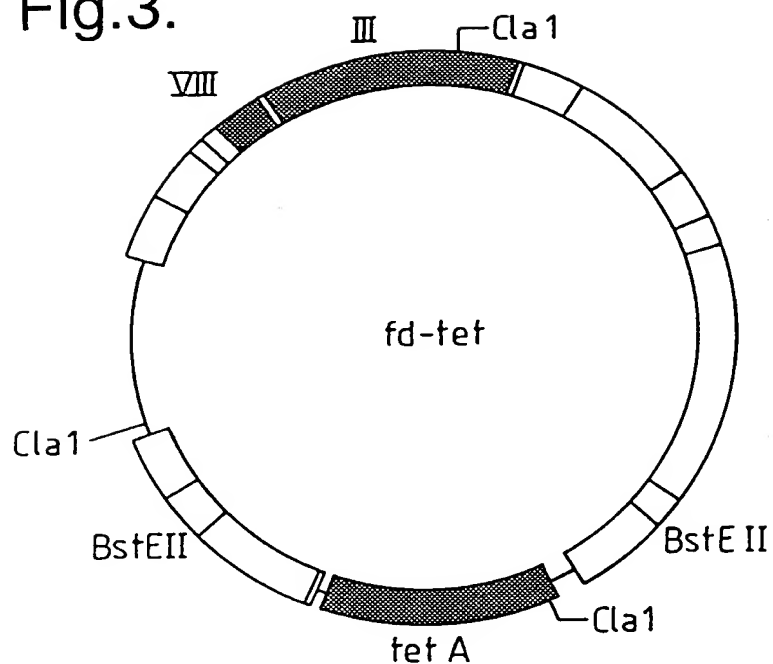


Fig.3.



fd - tet  
 ~  
 cleave with BstEII  
 ~  
 fill in with Klenow  
 ~  
 re-ligate  
 ↓  
 FDT6Bst  
 ~  
 in vitro mutagenesis (oligo 1)  
 ↓  
 FDTPs/Bs  
 ~  
 in vitro mutagenesis (oligo 2)  
 ↓  
 FDTPs/Xh

Fig.4a

Oligo 1 (1653)  
ACA ACT TTC AAC AGT TGA GGA GAC GGT GAC CGT AAG CTT CTG CAG TTG GAC CTG AGC (SEQ ID NO. 177)  
GGA GTG AGA ATA (1620)  
Oligo 2 (1653)  
ACA ACT TTC AAC AGT TTC CCG TTT GAT CTC GAG CTC CTG CAG TTG GAC CTG (SEQ ID NO. 178)  
(1704)  
Oligo 3 GTC GTC TTT CCA GAC GTT AGT (SEQ ID NO. 179)

Fig.4b

GENE III

GENE III

SIGNAL  
CLEAVAGE SITE

(1624)  
A TCT CAC TCC GCT  
(1650)  
GAA ACT GTT GAA AGT (SEQ ID NO. 180)

Q V Q L Q (SEQ ID NO. 1) V T V S S (SEQ ID NO. 2)  
B TCT CAC TCC GCT CAG GTC CAA CTG CAG AAG CTT ACG GTC ACC GTC TCC TCA ACT GTT GAA AGT (SEQ ID NO. 181)  
PstI BstEII

Q V Q L Q (SEQ ID NO. 1) L E I K R (SEQ ID NO. 3)  
C TCT CAC TCC GCT CAG GTC CAA CTG CAG GAG CTC GAG ATC AAACGG GAA ACT GTT GAA AGT (SEQ ID NO. 182)  
PstI XhoI

Fig.5a



Fig.5 b

E T V T I T C R A S G N I H N Y L A W Y  
GAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTAT  
550 560 570 580 590 600

Q Q K Q G K S P Q L L V Y Y T T T L A D  
CAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATTATACAACAACCTTAGCAGAT  
610 620 630 640 650 660

VKD1.3

G V P S R F S G S G S G T Q Y S L K I N  
GGTGTGCCATCAAGGTTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAAC  
670 680 690 700 710 720

S L Q P E D F G S Y Y C Q H F W S T P R  
AGCCTGCAACCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTGGAGTACTCCTCGG  
730 740 750 760 770 780

Myc Tag (TAG1)

T F G G G T K L E I K R E O K L I S E E  
ACGTTCCGGTGGAGGGACCAAGCTCGAGATCAAACGGGAACAAAACTCATCTCAGAAGAG  
790 800 810 820 830 840

XhoI

D L N \* \* (SEQ ID NO. 183)

GATCTGAATTAATAATGATCAAACGGTAATAAGGATCCAGCTCGAATTC (SEQ ID NO. 184)  
850 860 870 880

EcoRI

Fig.6.

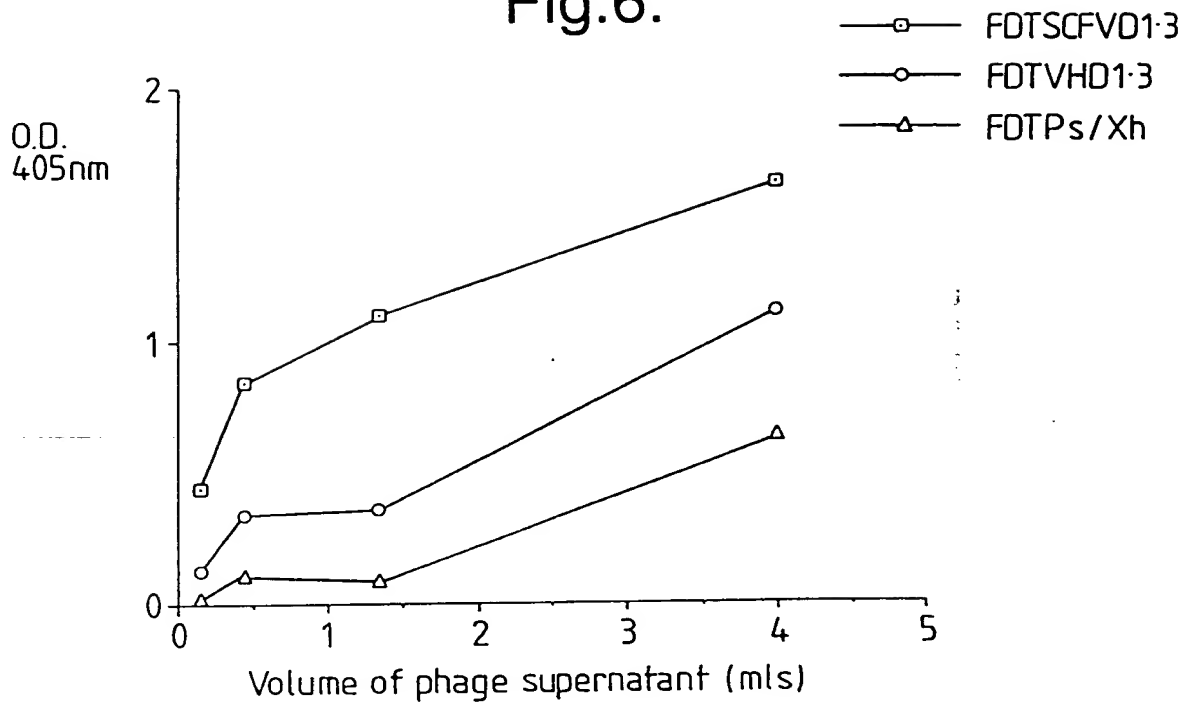


Fig.7.

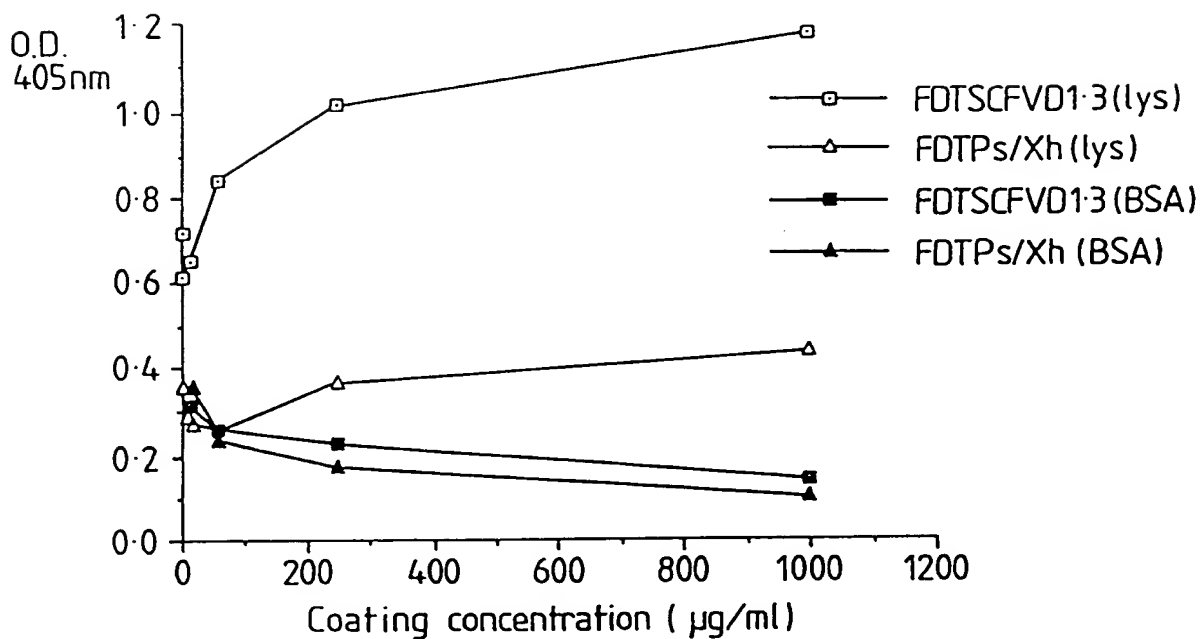






Fig.10a

M K Y L L P T A A  
GCATGCCAAATTCTATTTC AAGGAGACAGTCATAATGAAATACCTATTGCOCTACGGCAGCC  
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S  
GCTGGATTGTTATTACTGCTGCCCCAACCAGCGATGGCCCTGGTGCAGCTGCAGGAGTCA  
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F  
GGACCTGGCCTGGTGGCGCCCTCAGAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC  
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W  
TCATTAAACGGCTATGGTGTAAACTGGGTTCCGCCAGCCTCCAGGAAAGGGTCTGGAGTGG  
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L  
CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTACAGCTCTCAAATCCAGACTG  
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T  
AGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT  
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G  
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC  
370 380 390 400 410 420

Q G T T V T V S S A S T K G P S V F P L  
CAAGGCACCAACGGTCAACGTCTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG  
430 440 450 460 470 480

A P S S K S T S G G T A A L G C L V K D  
GCACCCCTCCTCCAAGAGCACCTCTGSGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGAC  
490 500 510 520 530 540



Fig.10b

Y F P E P V T V S W N S G A L T S G V H  
TACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGCGGTGCAC  
550 560 570 580 590 600

T F P A V L Q S S G L Y S L S S V V T V  
ACCTTCCCCGCTGTCTTACAGTCTCTAGCACTCTACTCCCTCAGCAGCGTGGTGACCGTG  
610 620 630 640 650 660

P S S S L G T Q T Y I C N V N H K P S N  
CCCTCCAGCAGCTTGGGCAACCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAGCAAC  
670 680 690 700 710 720

T K V D K K V E P K S S \* \* (SEQ ID NO. 187)  
ACCAAGGTGACACAAGAAAGTTCGCCCCAAATCTTCATAATAACCCGGGAGCTTGCATGCA  
730 740 750 760 770 780

M K Y L L P T A A A G L  
AATTCATTTTCAAGGACACAGTTCATTAATGAATACTTATTCCTAAGGCAGCCGCTGGAT  
790 800 810 820 830 840

L L L A A Q P A M A D I E L T Q S P A S  
TGTTTATTAAGCTGCTGCCCCAACCAGCGATGGCCGACATCGAGCTCACCAGTCTCCAGCCT  
850 860 870 880 890 900

L S A S V G E T V T I T C R A S G N I H  
CCCTTTCTGCGTCTGTGCGGAGAACTGTCAACATCACATGTGAGCAAGTGGGAATATTC  
910 920 930 940 950 960

N Y L A W Y Q Q K Q G K S P Q L L V Y Y  
ACAATTATTAGCATGGTATCAGCAGAAACAGGGAAAATCTCTCAGCTCCTGGTCTATT  
970 980 990 1000 1010 1020



Fig.10 c

T T T L A D G V P S R F S G S G S G T Q  
ATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTTCAGTGGCAGTGGATCAGGAACAC  
1030 1040 1050 1060 1070 1080

Y S L K I N S L Q P E D F G S Y Y C Q H  
AATATTCTCTCAAGATCAACAGCCTGCGCCTGAAGATTTTGGGAGTTATTACTGTCAAC  
1090 1100 1110 1120 1130 1140

F W S T P R T F G G G T K L E I K R T V  
ATTTTGGGAGTACTCTCGGACGTTGGTGGAGGCCACCAAGCTCGAGATCAAAACGGACTG  
1150 1160 1170 1180 1190 1200

A A P S V F I F P P S D E Q L K S G T A  
TGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGT  
1210 1220 1230 1240 1250 1260

S V V C L L N N F Y P R E A K V Q W K V  
CCTCTGTGTGTGTGCCCTGCTGAATACTTCTATCCCGAGAGGCCAAAGTACAGTGGGAGG  
1270 1280 1290 1300 1310 1320

D N A L Q S G N S Q E S V T E Q D S K D  
TGGATAACGCCCTCCAATGGGTAACTCCCGAGAGAGTGTACACAGAGCAGGACAGCAAGG  
1330 1340 1350 1360 1370 1380

S T Y S L S S T L T L S K A D Y E K H K  
ACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACA  
1390 1400 1410 1420 1430 1440

V Y A C E V T H Q G L S S P V T K S F N  
AAGTCTACGCCCTGCGAAGTCAACCATCAGGGCCTGAGCTCGCCCGTCAAAAGAGCTTCA  
1450 1460 1470 1480 1490 1500

R G E S \* \* (SEQ ID NO. 188)  
ACCGGGAGAGTGCATAGTAAGAATTC (SEQ ID NO. 189)  
1510 1520

Fig.10 d

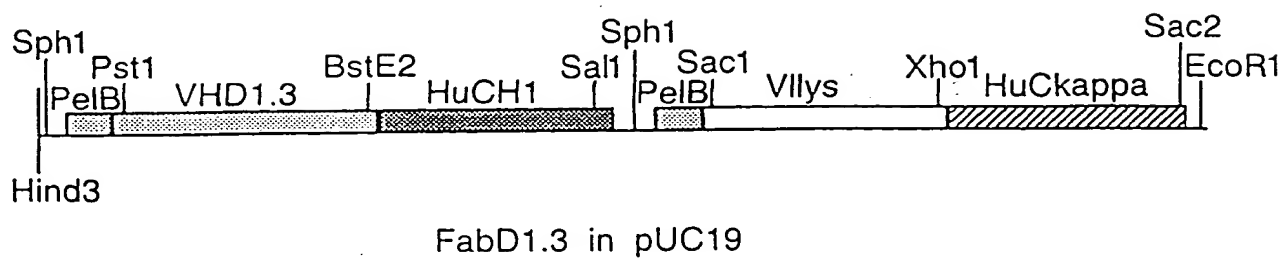


Fig.11.

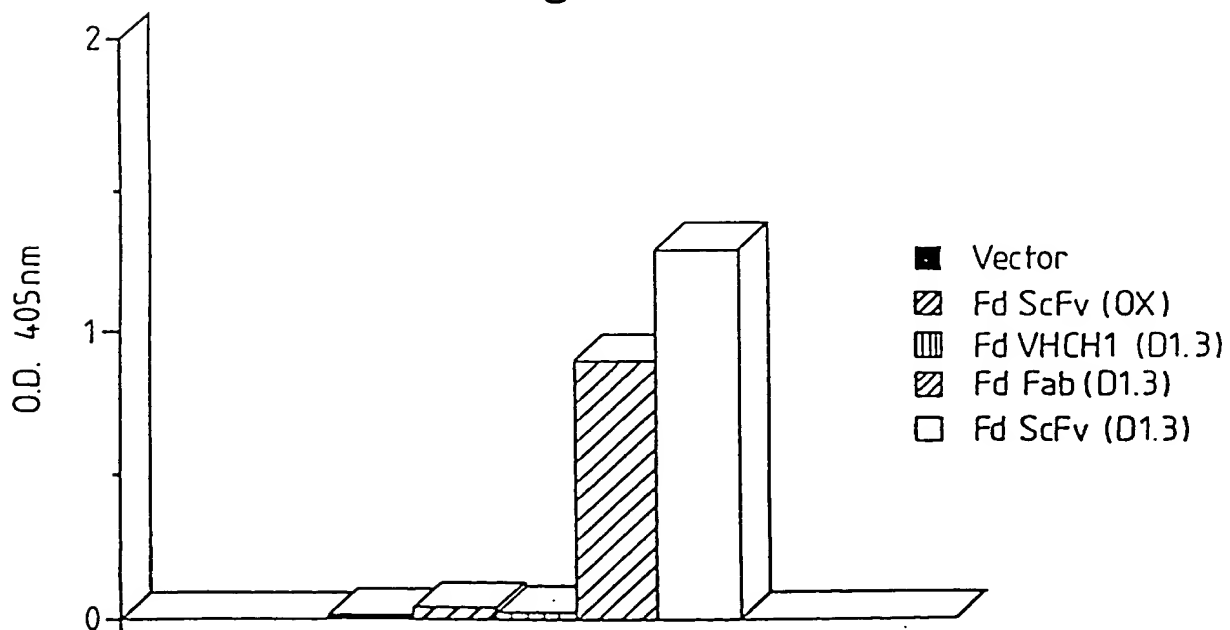




Fig.12a.

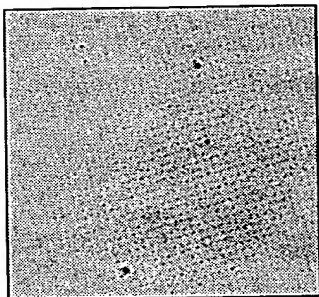


Fig.12b.

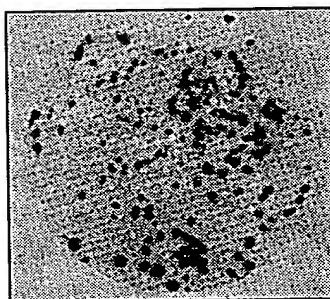




Fig.13.

Q V Q L Q E S G G L V Q P G G  
CAG GTG CAG CTG CAG GAG TCA GGA GGA GGC TTG GTA CAG CCT GGG GGT  
PstI  
S L R L S C A T S G F T F S N Y  
TCT CTG AGA CTC TCC TGT GCA ACT TCT GGG TTC ACC TTC AGT AAT TAC  
Y M G W V R Q P P G K A L E W L  
TAC ATG GGC TGG GTC CGC CAG CCT CCA GGA AAG GCA CTT GAG TGG TTG  
G S V R N K V N G Y T T E Y S A  
GGT TCT GTT AGA AAC AAA GTT AAT GGT TAC ACA ACA GAG TAC AGT GCA  
S V K G R F T I S R D N F Q S I  
TCT GTG AAG GGG CGG TTC ACC ATC TCC AGA GAT AAT TTC CAA AGC ATC  
L Y L Q I N T L R T E D S A T Y  
CTC TAT CTT CAA ATA AAC ACC CTG AGA ACT GAG GAC AGT GCC ACT TAT  
Y C A R G Y D Y G A W F A Y W G  
TAC TGT GCA AGA GGC TAT GAT TAC GGG GCC TGG TTT GCT TAC TGG GGC  
Q G T L V T v s s g g g g s g g g g s  
CAA GGG ACC CTG GTC ACC gtc tcc tca ggtggaggcggttcaggcgagggtggctct  
BstEII  
g g g g s d i E L T Q T P L S L P V  
ggcggtggcggtcgac atc GAG CTC ACC CAA ACT CCA CTC TCC CTG CCT GTC  
SacI  
S L G D Q A S I S C R S S Q S I  
AGT CTT GGA GAT CAA GCC TCC ATC TCT TGC AGA TCT AGT CAG AGC ATT  
V H S N G N T Y L E W Y L Q K P  
GTA CAT AGT AAT GGA AAC ACC TAT TTA GAA TGG TAC CTG CAG AAA CCA  
PstI  
G Q S P K L L I Y K V S N R F S  
GGC CAG TCT CCA AAG CTC CTG ATC TAC AAA GTT TCC AAC CGA TTT TCT  
G V P D R F S G S G S G T D F T  
GGG GTC CCA GAC AGG TTC AGT GGC AGT GGA TCG GGG ACA GAT TTC ACA  
L K I S R V E A E D L G V Y Y C  
CTC AAG ATC AGC AGA GTG GAG GCT GAG GAT CTG GGA GTT TAT TAC TGC  
F Q G S H V P Y T F G G G T K L  
TTT CAA GGT TCA CAT GTT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTC  
E I K R  
GAG ATC AAA CGG (SEQ ID NO. 190)  
XhoI (SEQ ID NO. 191)

Fig.14.

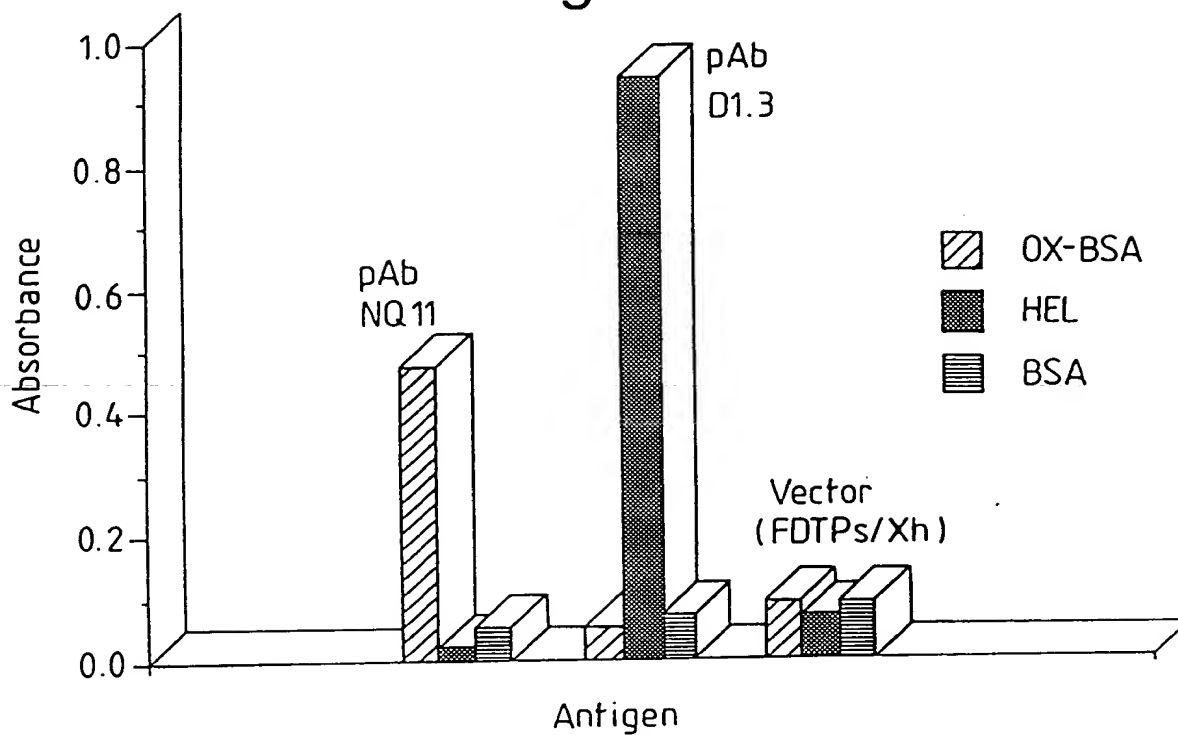


Fig.15.

5' END

TCT CAC AGT GCA CAA ACT GTT GAA CGG ACA CCA GAA ATG CCT GTT CTG (SEQ ID NO:193)  
 R T P E M P V L (SEQ ID NO:192)  
 ApaL1

3' END

K A A L G L K (SEQ ID NO:194)  
 AAA GCC GCT CTG GGG CTG AAA GCG GCC GCA GAA ACT GTT GAA AGT etc. (SEQ ID NO:195)  
 Not I

Fig.16a

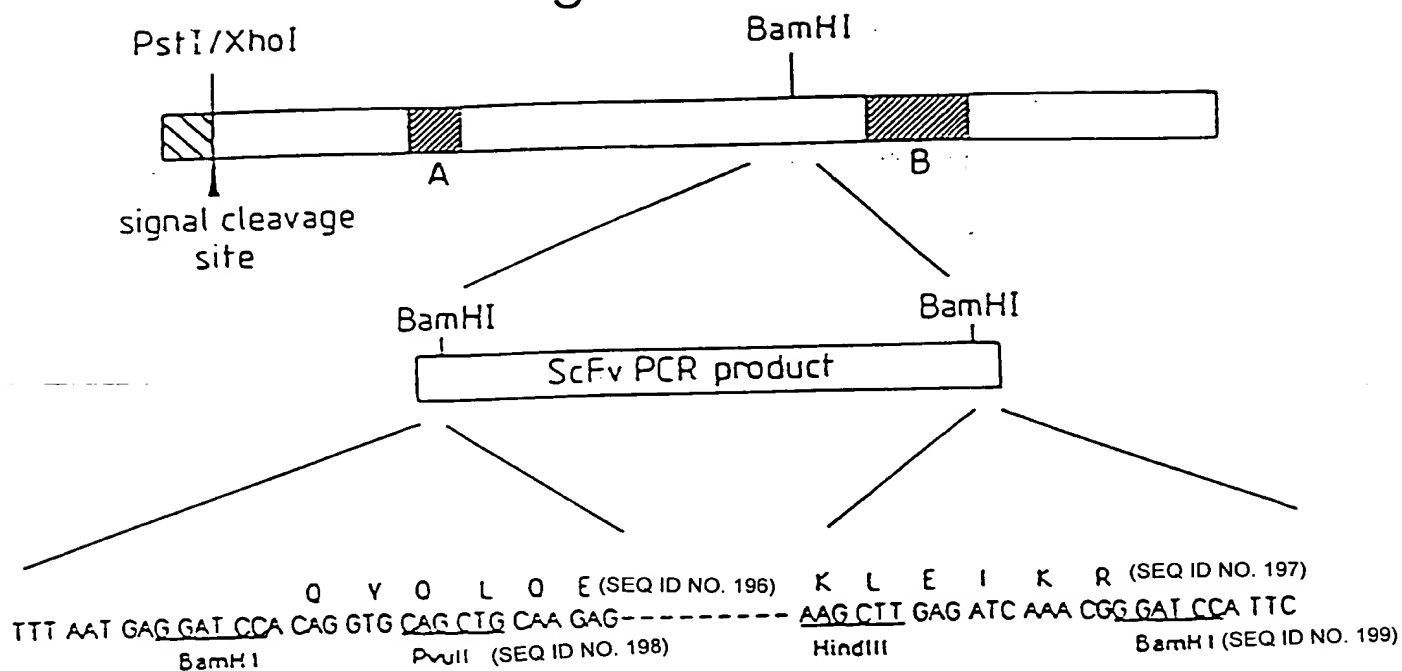


Fig.16b

A (1834) 5' GAG GGT GGT GGC TCT (SEQ ID NO. 200)  
 - - -C - - (SEQ ID NO. 201)  
 - - -C - - (SEQ ID NO. 202)  
 - - -C - ACT 3' (1839) (SEQ ID NO. 203)

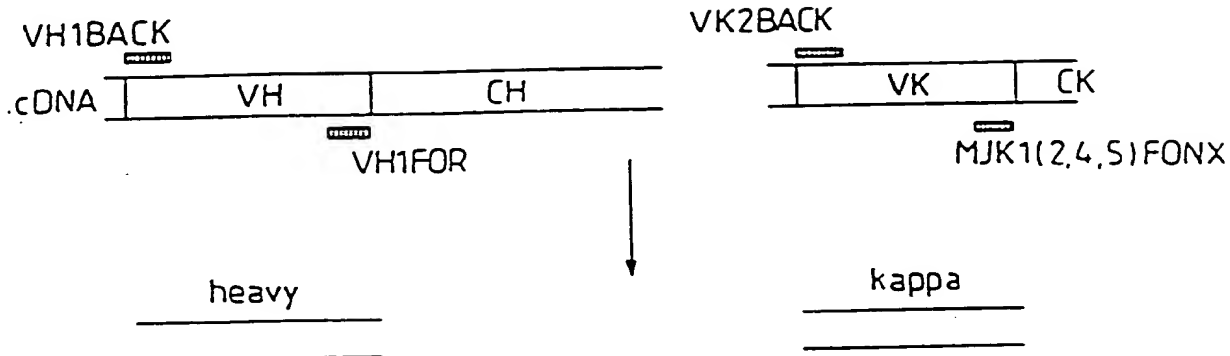
B (2284) 5' - GGC GGC GGC TCT (SEQ ID NO. 204)  
 - GGT GGT GGT - (SEQ ID NO. 205)  
 - - GGC GGC - (SEQ ID NO. 206)  
 GAG - - GGC - (SEQ ID NO. 207)  
 - - - GGT - (SEQ ID NO. 208)  
 - - - GGC - (SEQ ID NO. 209)  
 - - - GGT - (SEQ ID NO. 210)  
 - - - GGC - 3' (2379) (SEQ ID NO. 211)

Reverse complement of mutagenic  
 oligo G3Bamlink  
 5' GAG GGT GGC GGA TCC (SEQ ID NO. 212)  
 GAG GGT GGC GG 3' (SEQ ID NO. 213)

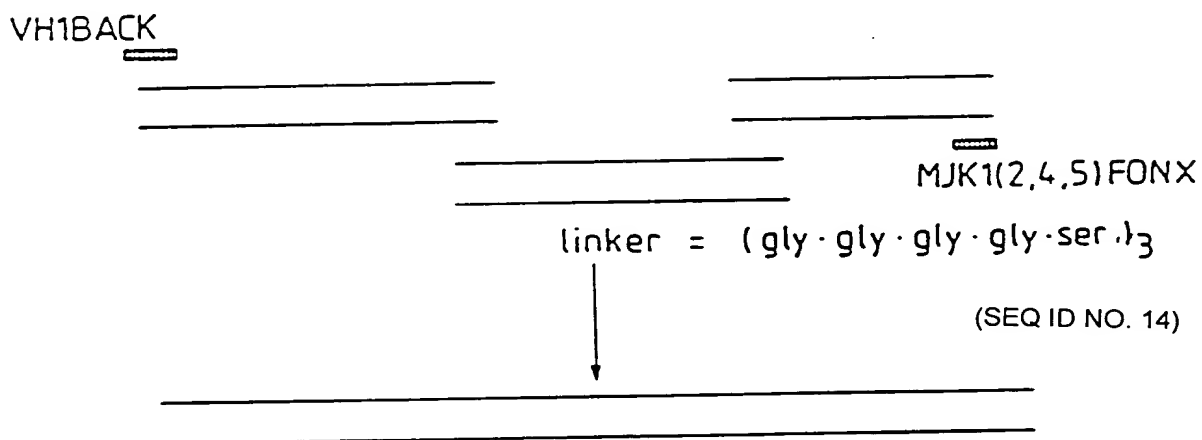


Fig.17.

1) PRIMARY PCR



2) ASSEMBLY PCR



3) ADDING RESTRICTION SITES

VHBKAPA10

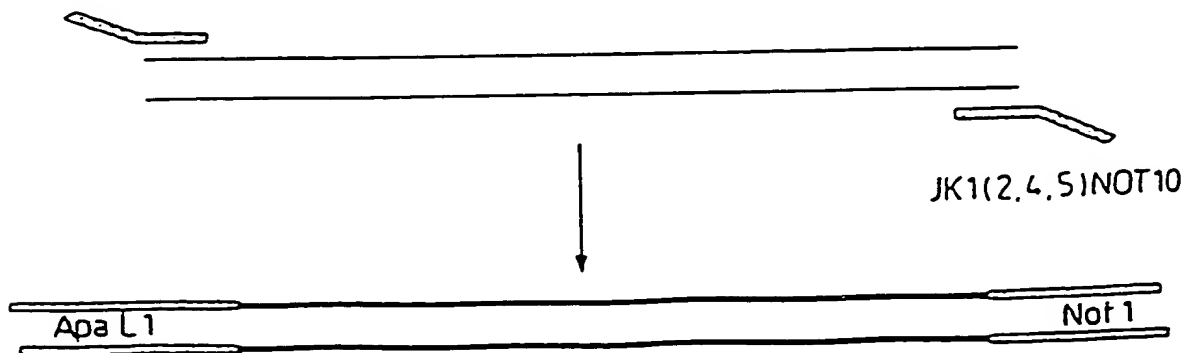




Fig.18.

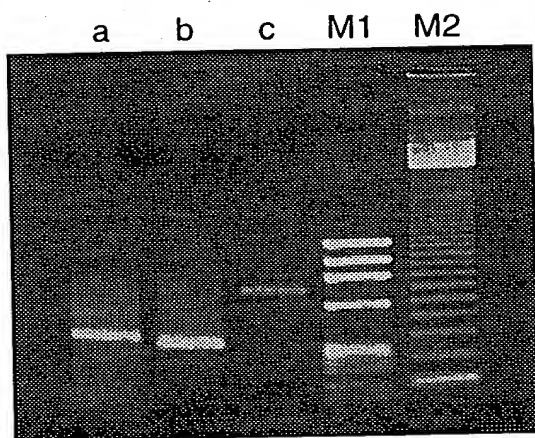


Fig.19.

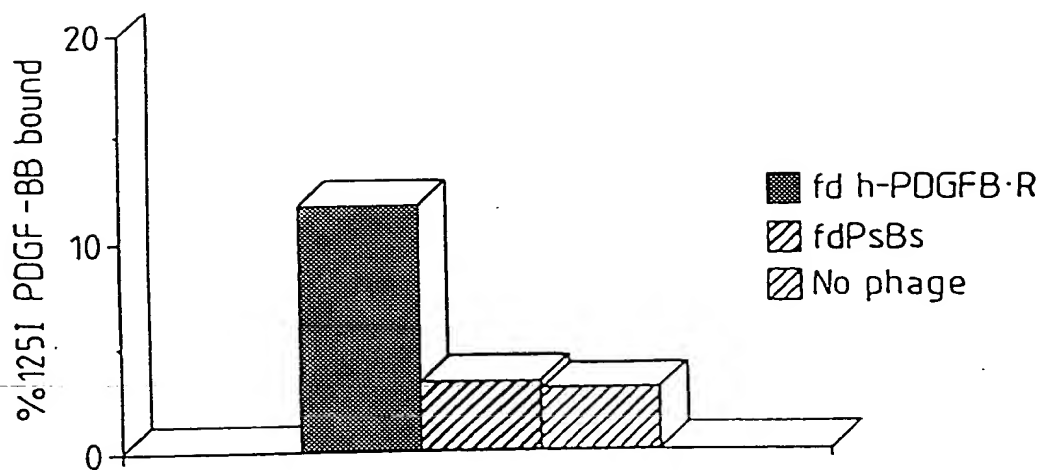


Fig.20.

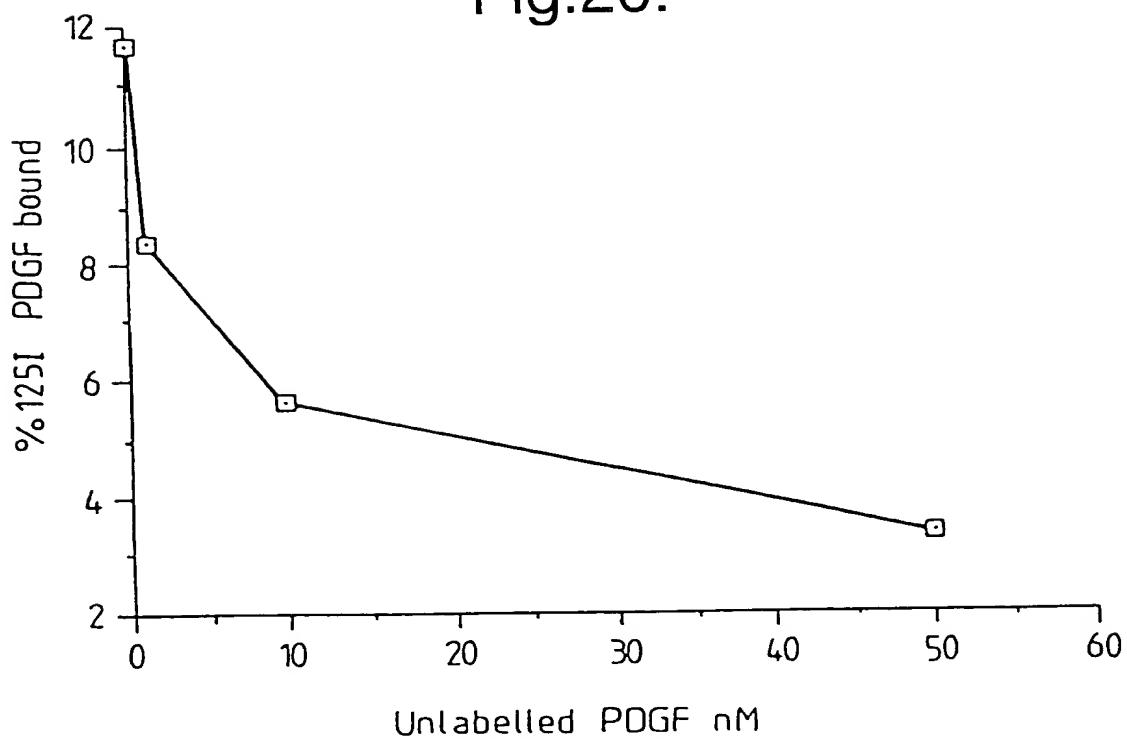


Fig.21.

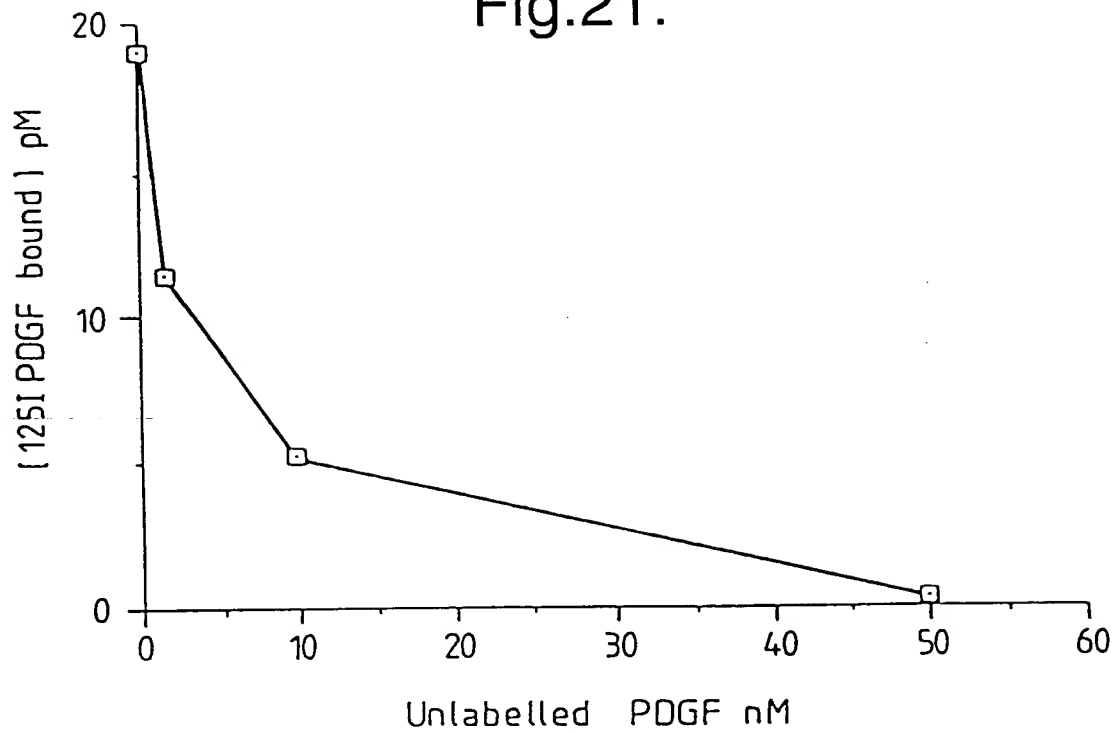


Fig.22.

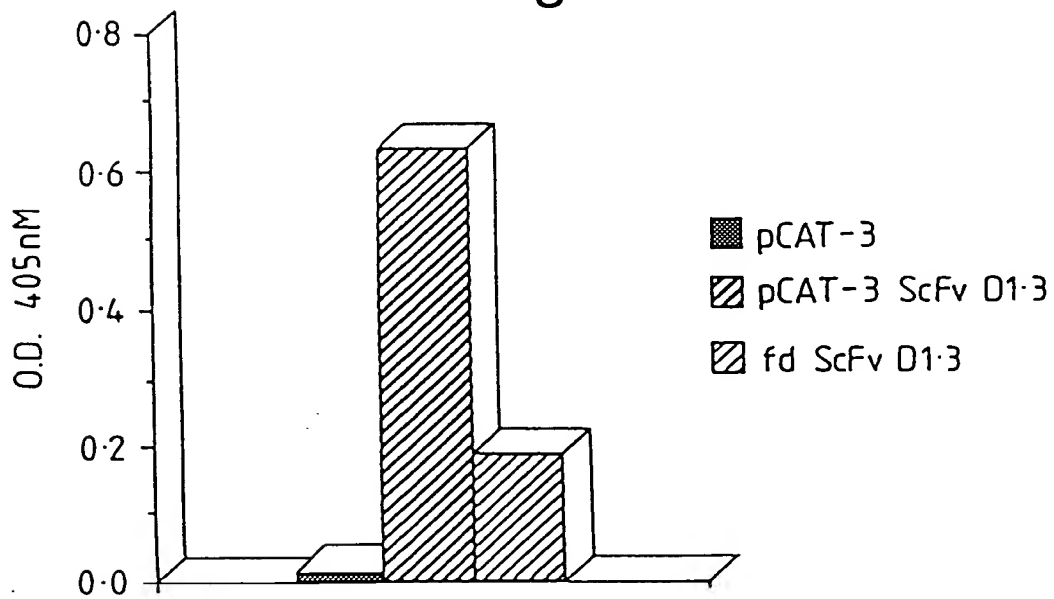




Fig.23a

d  
M

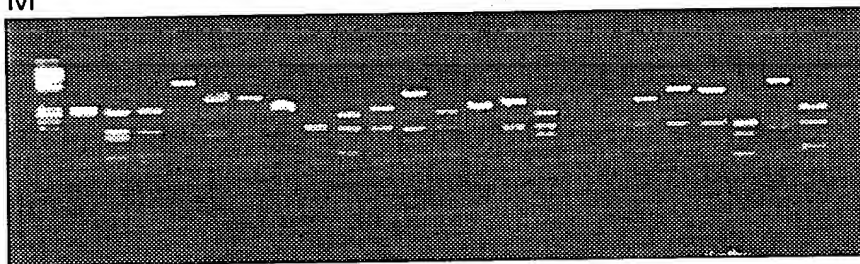
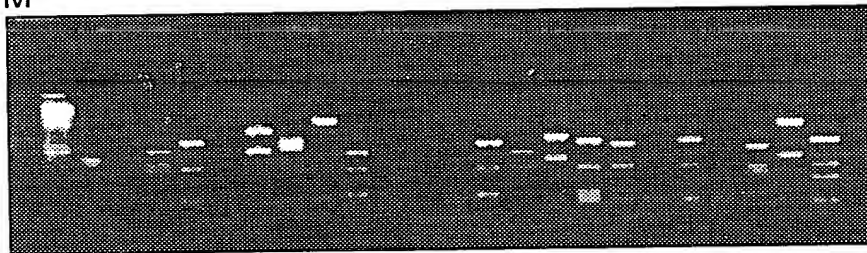


Fig.23b

M





VH sequences

Fig.24a

from combinatorial library:

	CDR1	CDR2	CDR3		(SEQ ID NO. 214)
A	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9 x4	(SEQ ID NO. 215)
B	QVQLQSGOELAKPGAEVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9 x9	(SEQ ID NO. 216)
C	QVQLQSGOELVXPGAGVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9 x3	(SEQ ID NO. 217)
D	QVQLQSGOELVXPGAGVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9 x3	(SEQ ID NO. 218)
E	QVQLQSGOELVXPGAGVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9 x3	(SEQ ID NO. 219)
F	QVQLQSGOELVXPGAGVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9 x3	(SEQ ID NO. 220)
G	QVQLQSGOELVXPGAGVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9 x3	(SEQ ID NO. 221)
H	QVQLQSGOELVXPGAGVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9 x3	(SEQ ID NO. 222)

from hierarchical library Vh-rep x Vh-d:

	CDR1	CDR2	CDR3		(SEQ ID NO. 223)
I	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 224)
J	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 225)
K	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 226)
L	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 227)
M	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 228)
N	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 229)
O	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 230)
P	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 231)
Q	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 232)
R	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 233)
S	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 234)
T	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 235)
U	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 236)
V	QVQLQSGOELARPGASVTHSKASGTTT	YINPSTGYTETNPKFKD	KATLTADKSSSTA YHQLSSLTSED8AVTYCAR	WGQCTTVTVS9	(SEQ ID NO. 237)



Fig.24b

Vx sequences

from combinatorial library:

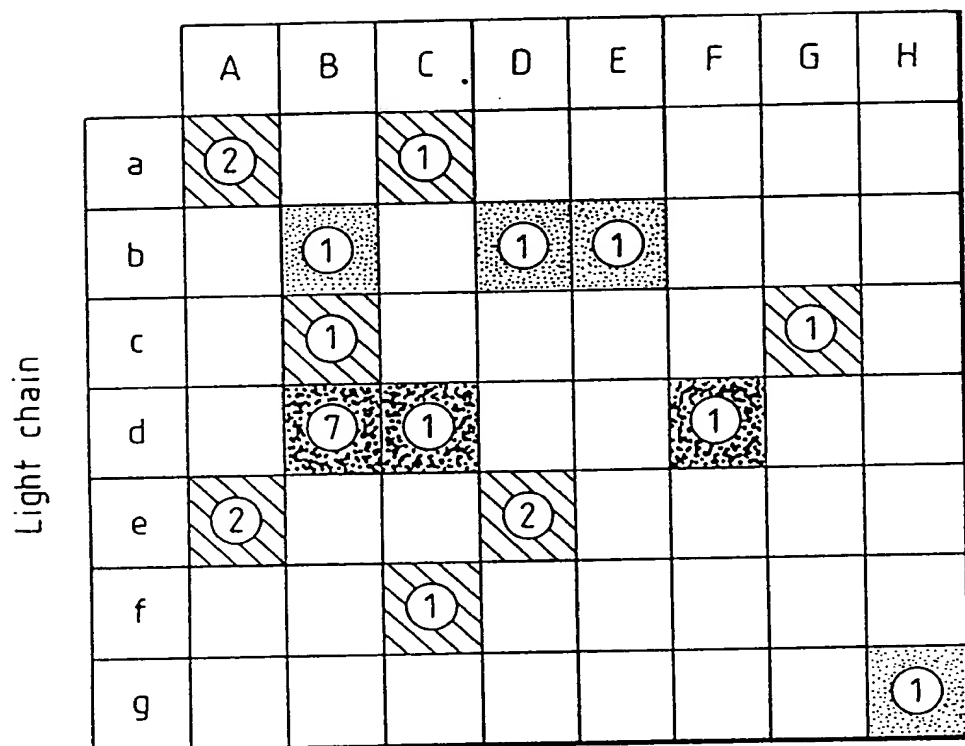
	CDR1	CDR2	CDR3			
a	DIELTQSP5SLASLGERVSLTC	WLOQKPGSIPKRLIY	QVPAKFSGSGSGTGYSLTISSEEDVADYYC	FGAGTKLEIKRA x3	V	ox-1ike (SEQ ID NO. 236)
b	DIELTQSPAIHSAASPGKVTTC	MYQOKSGASPKVMIIY	QVPAKFSGSGGCTGYSLTISSEVEDAATYYC	FGAGTKLEIKRA x3	IV	ox-1ike (SEQ ID NO. 237)
c	DIELTQSPPTTHAASPGKVTTC	MYQOKPGFSPKLLIY	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA x3	IV	ox-1ike (SEQ ID NO. 238)
d	DIELTQSPPTTHAASPGKVTTC	MYQOKPGFSPKLLIS	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA x9	IV	ox-1ike (SEQ ID NO. 239)
e	DIELTQSPAIHSAASPGKVTTC	MYQOKPGFSPKLMIIY	QVPAKFSGSGGCTGYSLTISSEVEDAATYYC	FGAGTKLEIKRA x4	VI	ox-1ike? (SEQ ID NO. 240)
f	DIELTQSPAIHSAASPGKVTTC	MYQOKSGTSPKRMIIY	QVPAKFSGSGGCTGYSLTISSEVEDAATYYC	FGAGTKLEIKRA	VI	Wox1 (SEQ ID NO. 241)
g	DIELTQSPAIHSAASPGKVTTC	MYQOKPGASPKRMIIY	QVPAKFSGSGGCTGYSLTISSEVEDAATYYC	FGAGTKLEIKRA	VI	ox-1ike? (SEQ ID NO. 242)

from hierarchical library VII-B x Vx-rep:

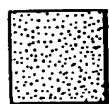
h	DIELTQSPAIHSAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTISSEVEDAATYYC	FGAGTKLEIKRA x4	IV/VI	Wox1 (SEQ ID NO. 243)
i	DIELTQSPAIHSAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTISSEVEDAATYYC	FGAGTKLEIKRA	V	ox-1ike? (SEQ ID NO. 244)
j	DIELTQSPPTTHAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA	V	ox-1ike (SEQ ID NO. 245)
k	DIELTQSPPTTHAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA	V	ox-1ike (SEQ ID NO. 246)
l	DIELTQSPPTTHAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA	V	ox-1ike (SEQ ID NO. 247)
m	DIELTQSPPTTHAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA	V	ox-1ike (SEQ ID NO. 248)
n	DIELTQSPPTTHAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA	V	ox-1ike (SEQ ID NO. 249)
o	DIELTQSPAIHSAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA x3	V	ox-1ike (SEQ ID NO. 250)
p	DIELTQSPAIHSAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA	IV/VI	Wox1 (SEQ ID NO. 251)
q	DIELTQSPAIHSAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA	IV/VI	Wox1 (SEQ ID NO. 252)
r	DIELTQSPAIHSAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA	IV/VI	Wox1 (SEQ ID NO. 253)
s	DIELTQSPAIHSAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA	IV/VI	ox-1ike (SEQ ID NO. 254)
t	DIELTQSPAIHSAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA	IV/VI	ox-1ike (SEQ ID NO. 255)
u	DIELTQSPAIHSAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA	IV/VI	ox-1ike (SEQ ID NO. 256)
v	DIELTQSPAIHSAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA	IV/VI	ox-1ike (SEQ ID NO. 257)
w	DIELTQSPAIHSAASPGKVTTC	SASSSVSTMI	QVPAKFSGSGGCTGYSLTIGTMEAEADVATYYC	FGAGTKLEIKRA	IV/VI	ox-1ike (SEQ ID NO. 258)

Fig.25.

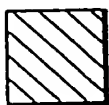
HEAVY CHAIN



OD<sub>405nm</sub> in ELISA



0.2-0.9



0.9-2.0



>2.0



Fig.26(a).

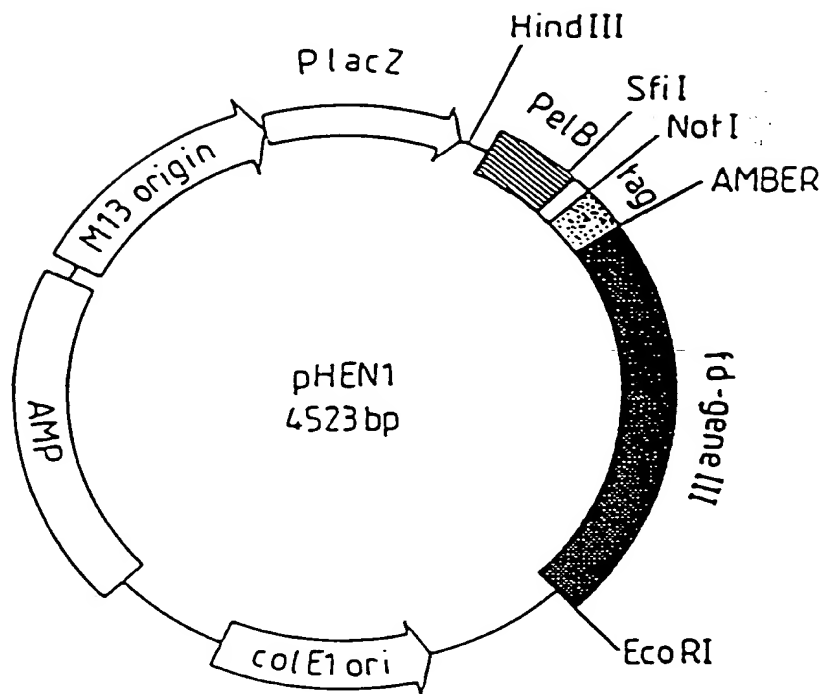


Fig.26(b).

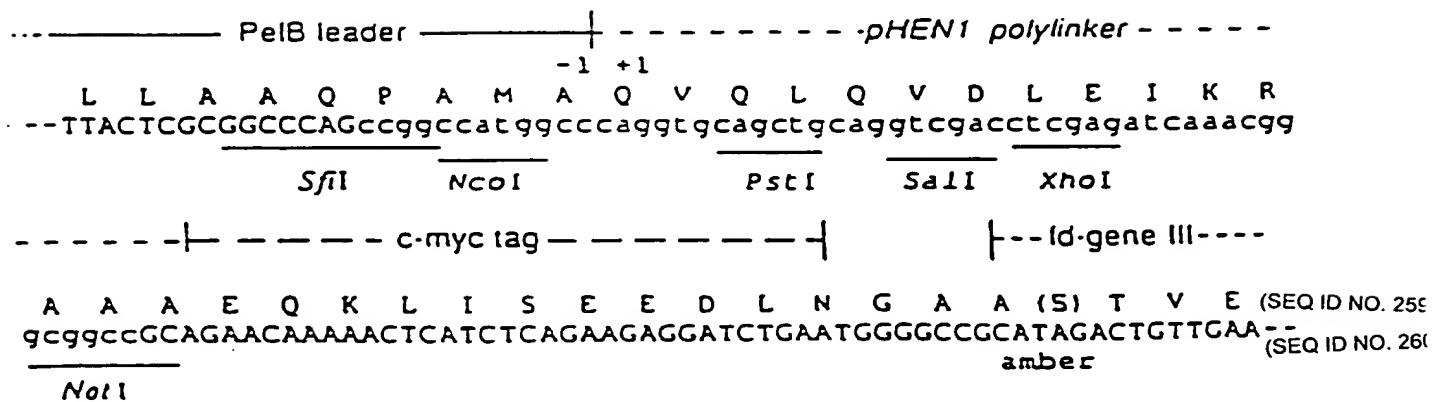


Fig.27.

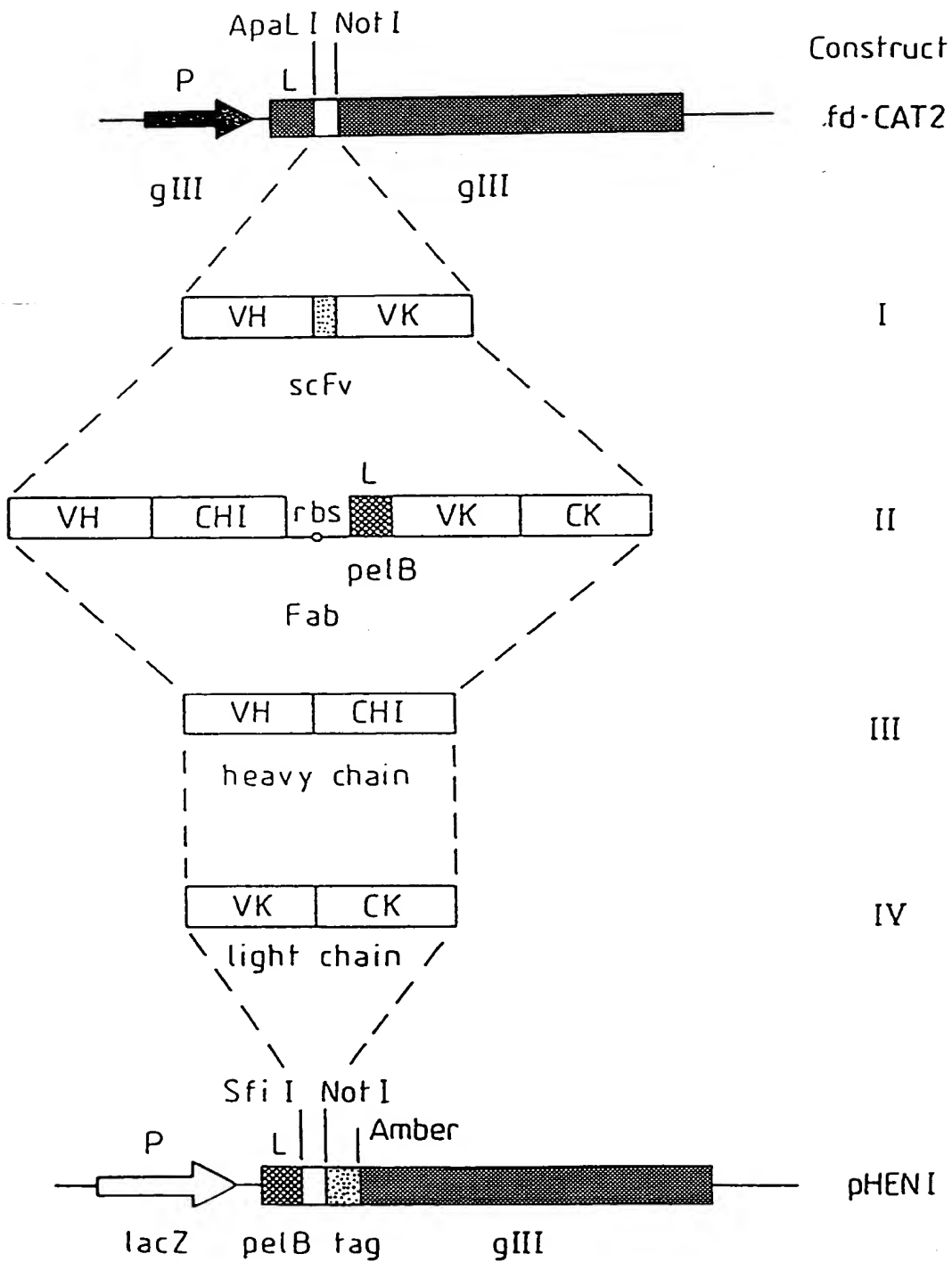


Fig.28.

Fab

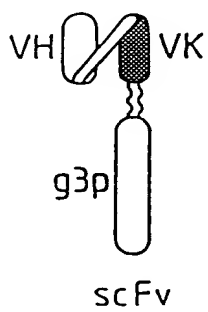
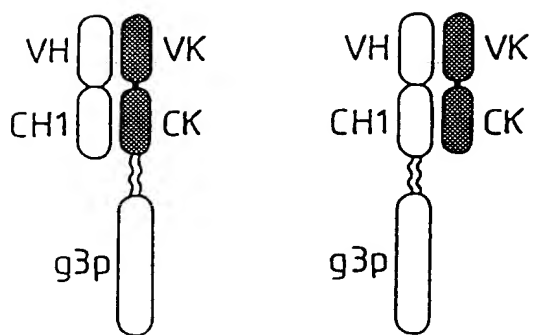




Fig.29.

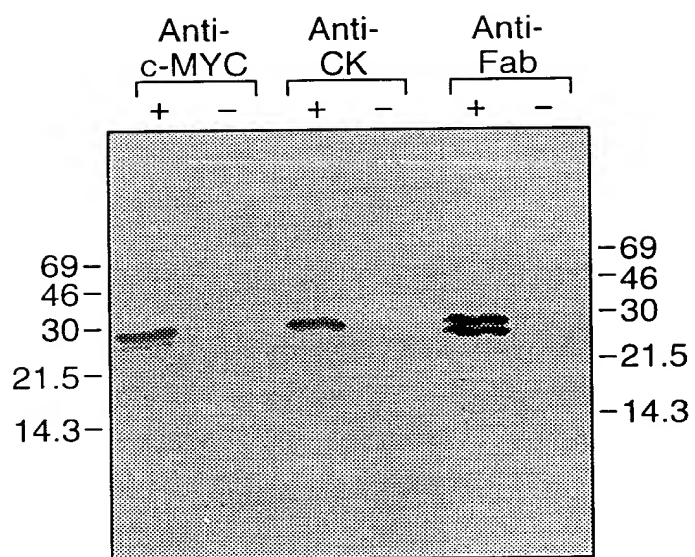




Fig.30.

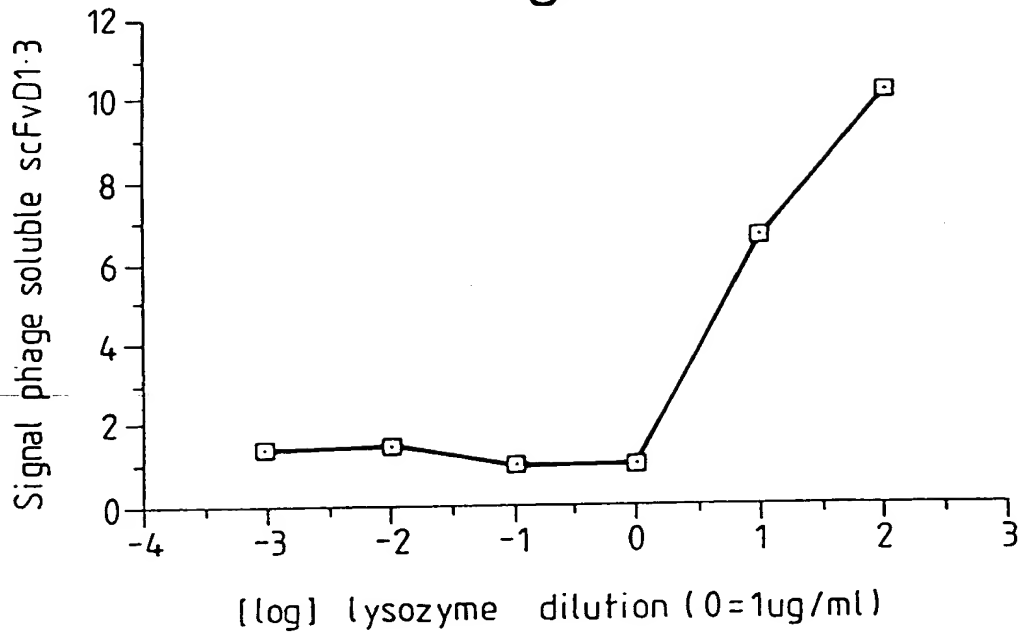


Fig.31.

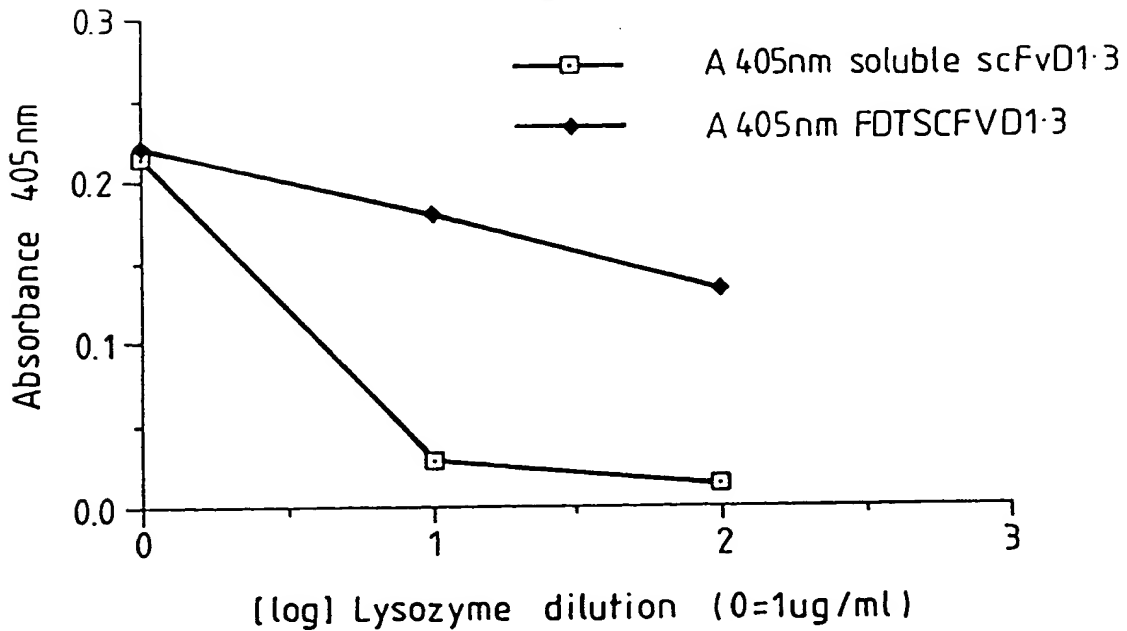


Fig.32.

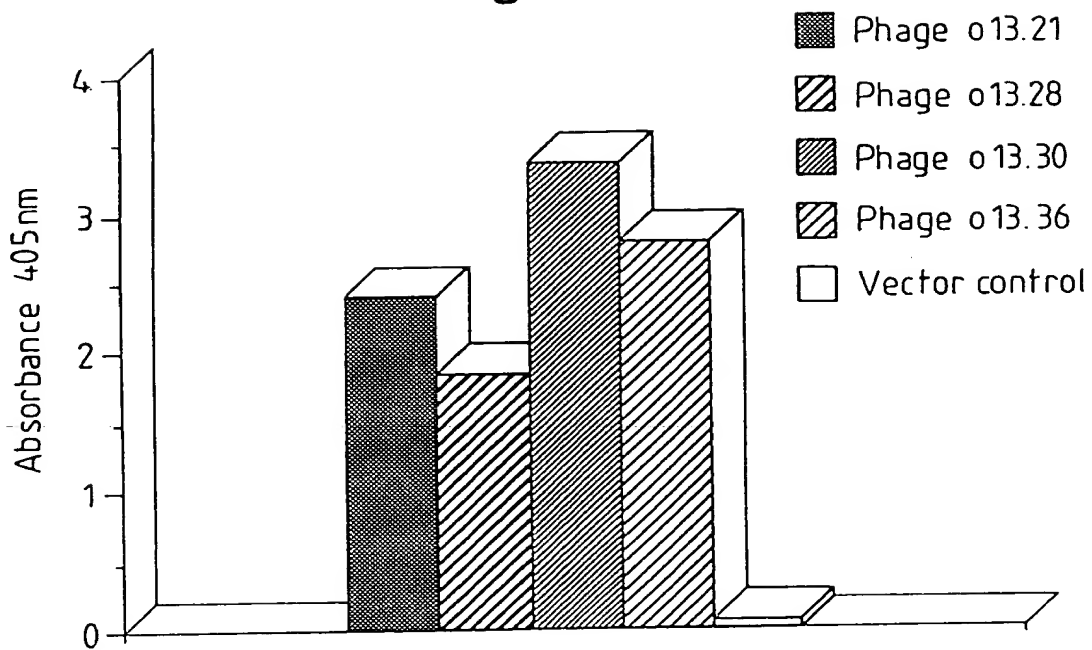


Fig.33.

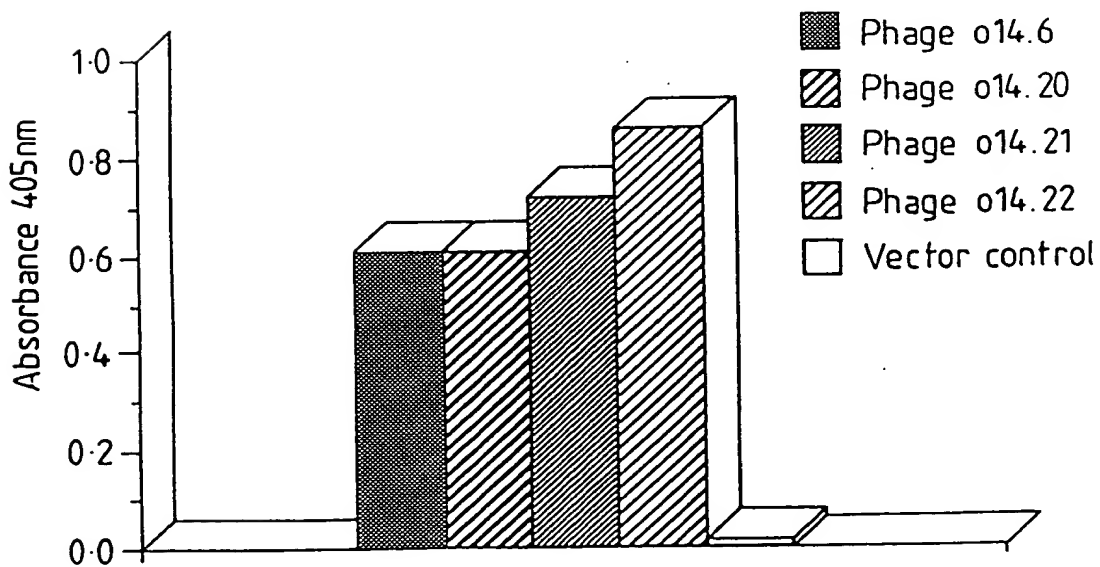




Fig.34.

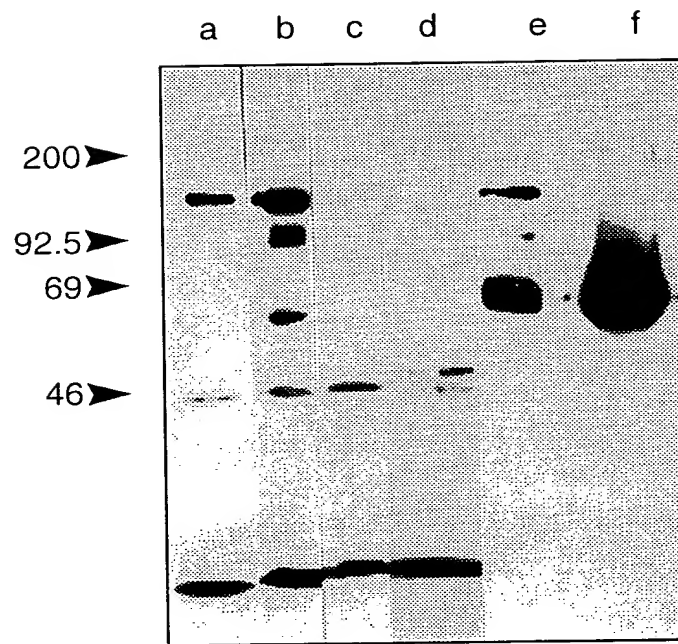


Fig.35A.

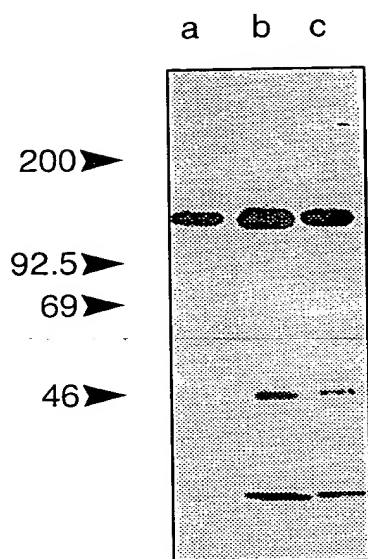


Fig.35B.

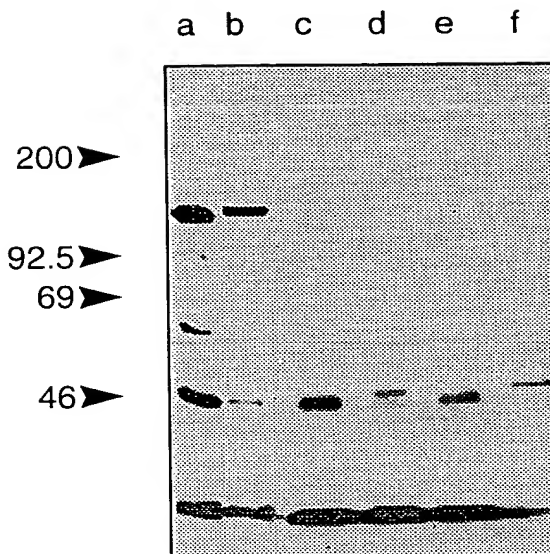


Fig.36.

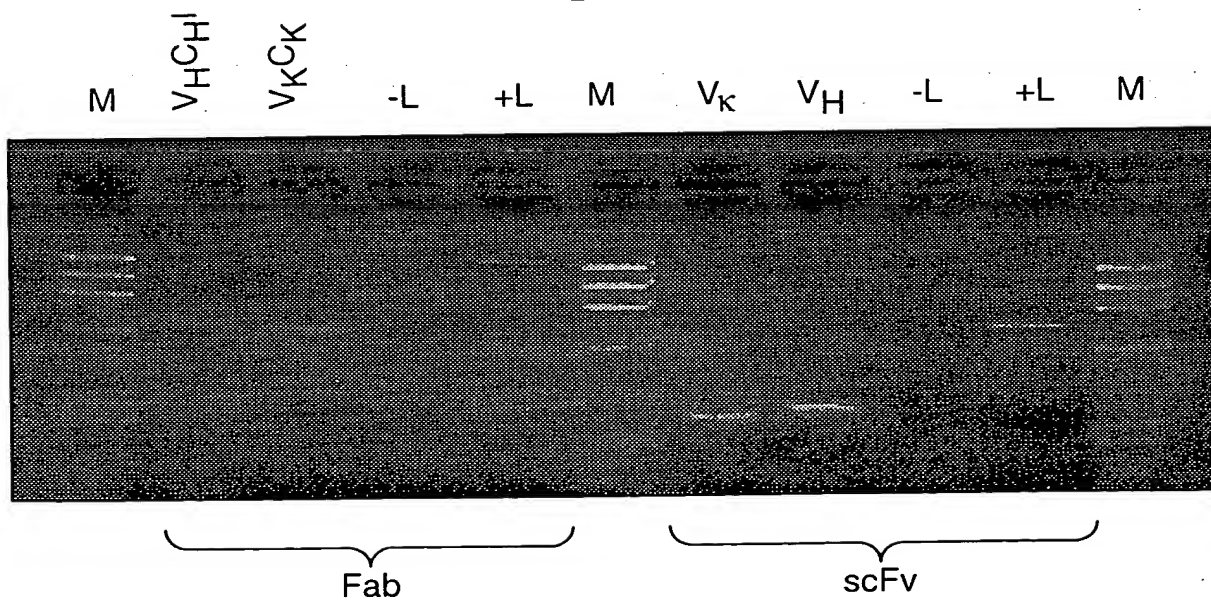


Fig.37.

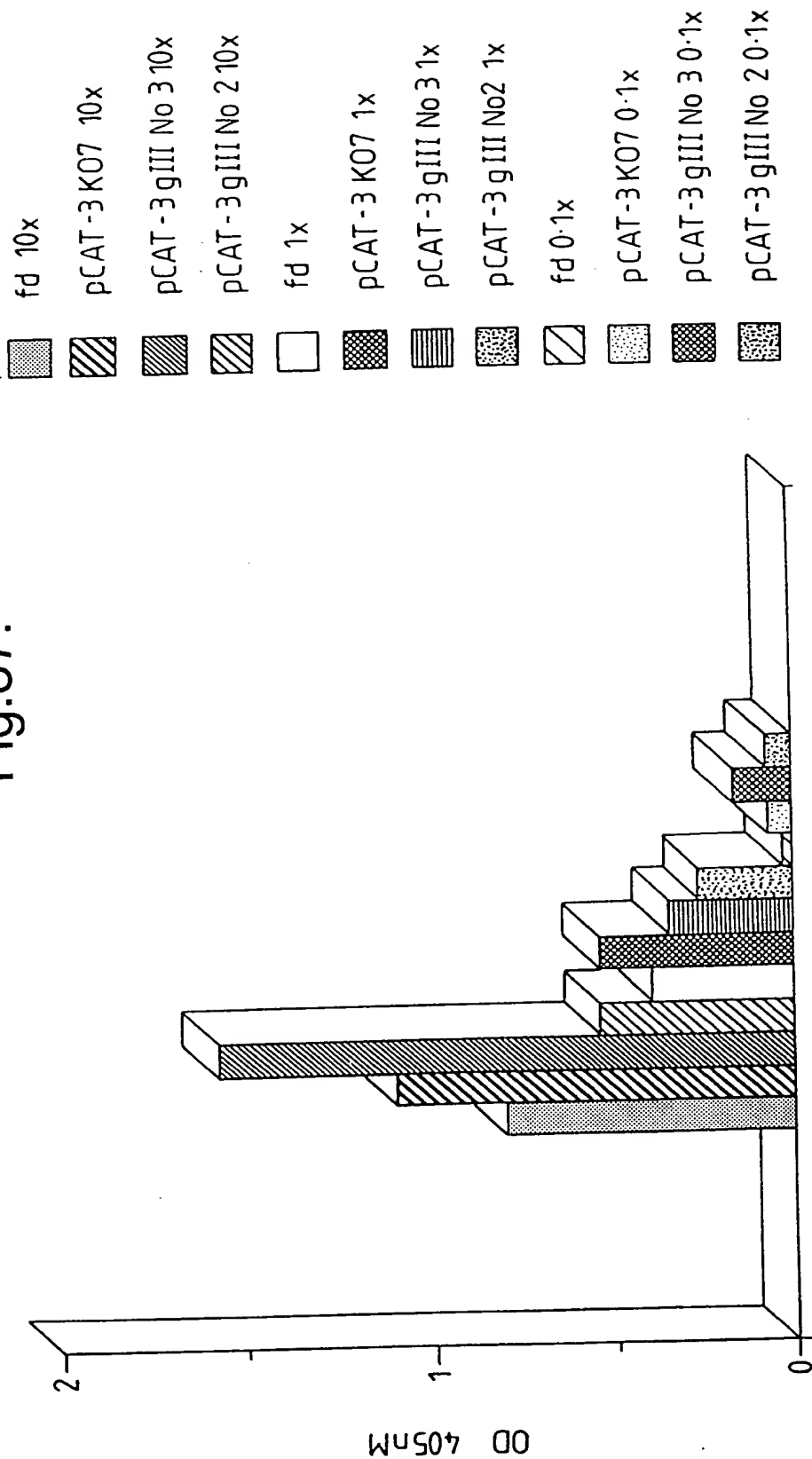




Fig.38A.

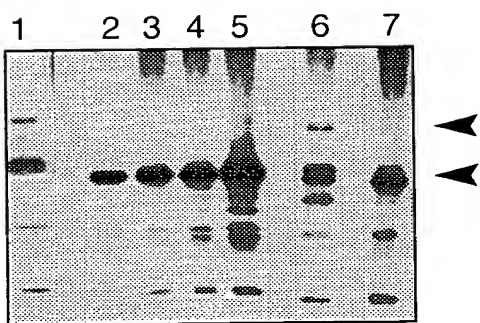


Fig.38B.

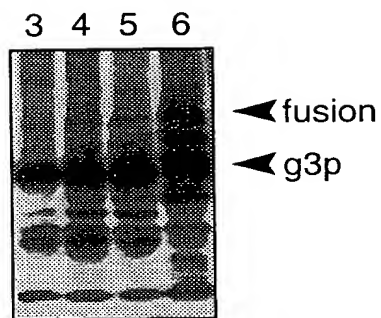


Fig.39.

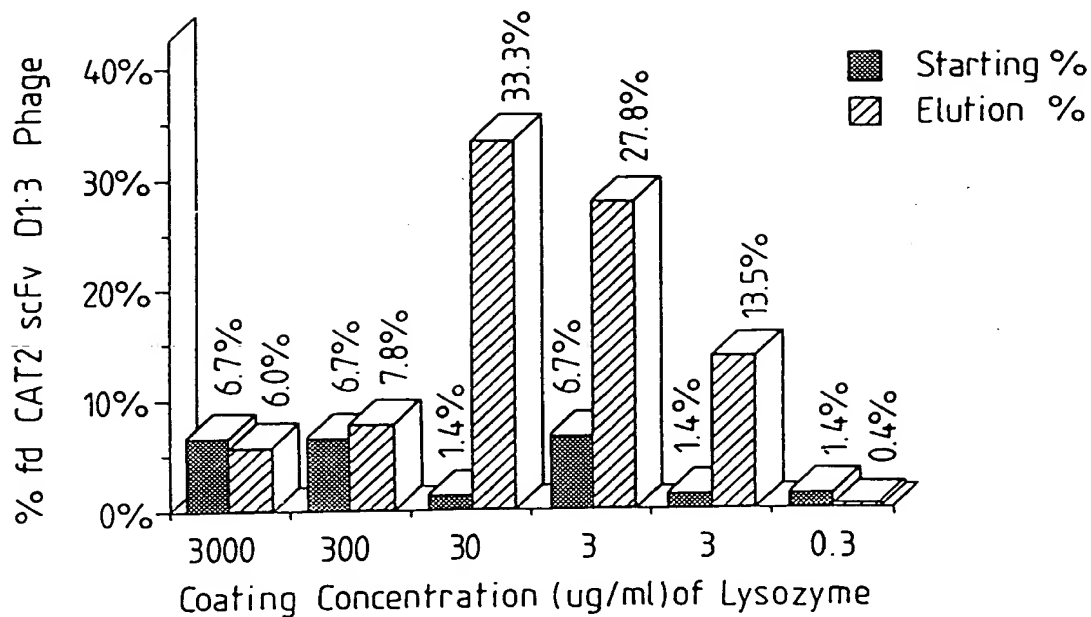


Fig.40.

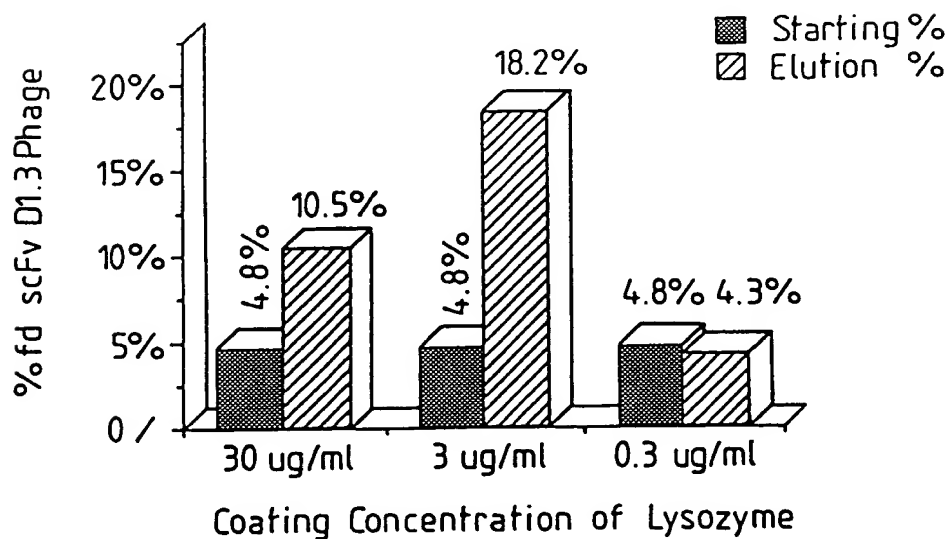




Fig.41.

1 2

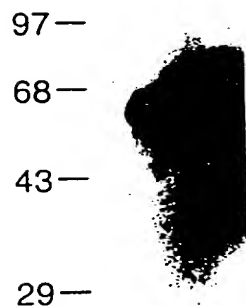


Fig.42.

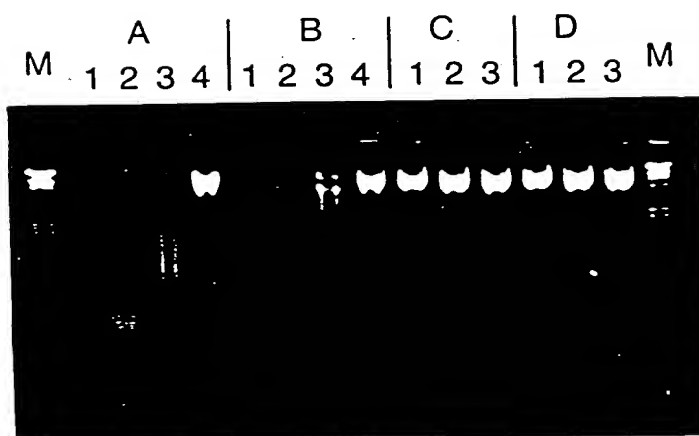




Fig.43.

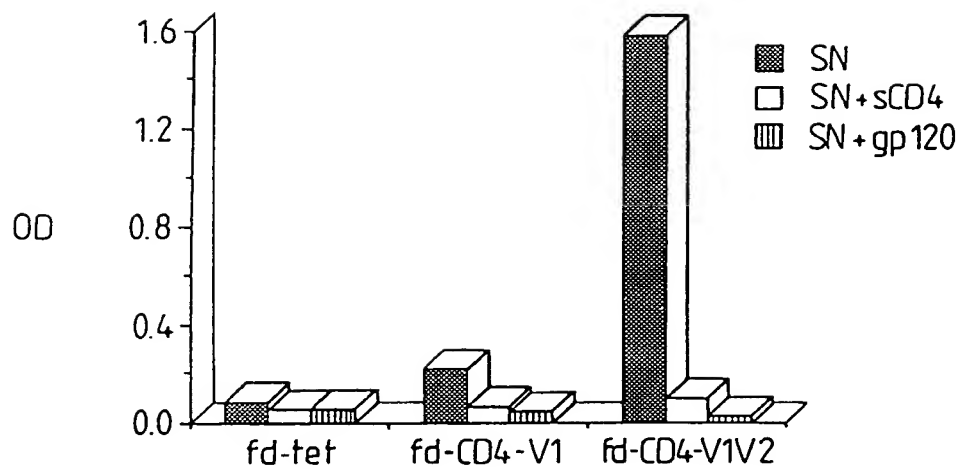


Fig. 44a

10	20	30	40	50	60	70	80	90
TTCTATTCTCACAGTGCACAGGTCACAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCCTGGGGCTTCAGTGAAGCTGTCCCTGCAAGGCT								
AAGATAAGAGTGTACGTGTCAGGTCGACGTCGACACCCGACTCGAACACTTCGGACCCCGAAGTCACTTCGACACGACGTTCCCGA								
pheTyrSerHisSerAlaGlnValGlnLeuGlnSerGlyAlaGluLeuValLysProGlyAlaSerValLysLeuSerCysLysAla								
100	110	120	130	140	150	160	170	180
TCTGGCTACACCTTCACCACTACTGGATGCACCTGGGTGAAGCAGAGCCCTGGACGAGCCCTTGAGTGGATTGGAAGGATTGATCCTAAT								
AGACCGATGTGGAGTGGTCGATGACCTACGTGACCCACTTCGTCTCCGGACCTGCTCCGGAACCTCACCTAACCTTCCTAAGTACAGGATTA								
SerGlyTyrThrPheThrSerTyrTrpMetHisTrpValLysGlnArgProGlyArgGlyLeuGluTrpIleGlyArgIleAspProAsn								
190	200	210	220	230	240	250	260	270
AGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAACCCCTCCAGCACAGCCCTACATGCAGCTCAGC								
TCACCAACCATGATTCACTCTCAAGTCTCTCGTTCGGGTGACTGACATCTGTTTGGGAGGTCGTGTCGGATGTACGTCGAGTCG								
SerGlyGlyThrLysTyrAsnGluLysPheLysSerLysAlaThrLeuThrValAspLysProSerSerThrAlaTyrMetGlnLeuSer								
280	290	300	310	320	330	340	350	360
AGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGCAAGATACGACTACGGTAGTAGCTACTACTTTGACTACTGGGGCCCAAGGGACC								
TCGGACTGTAGACTCCTGAGACGCCAGATAATAACAGTTCTATGCTGATGCCATCATCGATGATGAAGTATGATGACCCCGGTTCCCTGG								
SerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgTyrAspTyrGlySerSerTyrTyrPheAspTyrTrpGlyGlnGlyThr								
370	380	390	400	410	420	430	440	450
ACGGTCACCGTCTCCTCAGGTGGAGGCGGTTACAGCGGAGGTGGCTCTGGCGGTGGCGGATCCAGGCTGTTGGGACACACAGGAATCTGCA								
TGCCAGTGGCAGAGGAGTCCACCTCCGCCAAGTCCGCCCTCCACCGAGACCCGCCACCGCTAGGGTCCGACAAACCTGTGTCTTAGACGT								
ThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlnAlaValGlyThrGlnGluSerAla								
460	470	480	490	500	510	520	530	540
CTCACCAACATCACCTGGTGAACACAGTCACACTACTGTCCGCTCAAGTACTGGGGCTGTACAACTAGTAACATACTATGCCAACTGGGTCCCAA								
GAGTGGTGTAGTGACCACTTGTGTCAGTGTGAGTGAACAGCGAGTTTCATGACCCCGACAAATGTTGATCATTTGATACGTTGACCCAGGTT								
LeuThrThrSerProGlyGluThrValThrLeuThrCysArgSerSerThrGlyAlaValThrThrSerAsnTyrAlaAsnTrpValGln								
550	560	570	580	590	600	610	620	630
GAAAAACAGATCATTTATTCACTGGTCTAATAGGTGGTACCAACAACCGAGCTCCAGGTGTTCTCTGCCAGATTCTCAGGCTCCCTGATT								
CTTTTGGTCTAGTAAATAAGTGACCAAGATTATCCACCATGGTTGTTGGCTCGAGGTCCACAAGGACGGTCTAAGAGTCCGAGGGACTAA								
GluLysProAspHisLeuPheThrGlyLeuIleGlyGlyThrAsnAsnArgAlaProGlyValProAlaArgPheSerGlySerLeuIle								



Fig.44 b

640 650 660 670 680 690 700 C G 710 720  
GGAGACAAGGCTGCCCTCACCATCACAGGGGCACAGACTGAGGATGAGGCATATATTTCTGTGCTCTATGGTACAGCAACCATTTGGGTG  
CCTCTGTTCCGACGGGAGTGTGTCCCGTGTCTGACTCCTACTCCGTTATATAAGACACGAGATACCATGTGCTTGGTAACCCAC  
GlyAspLysAlaAlaLeuThrIleThrGlyAlaGlnThrGluAspGluAlaIleTyrPheCysAlaLeuTrpTyrnberAsnHisTrpVal  
730 740 750 760 770  
TTCGGTGGAGGAACCAAACTGACTGTCCCTCGAGATCANAACGGGGCGGCCGC (SEQ ID NO. 261)  
AAGCCACCTCCTTGTTGACTGACAGGAGCTCTAGTTGCCCGCCGGCG  
pheGlvGlyGlyThrLysLeuThrValLeuGluIleLysArgAlaAla (SEQ ID NO. 262)

Fig.45.

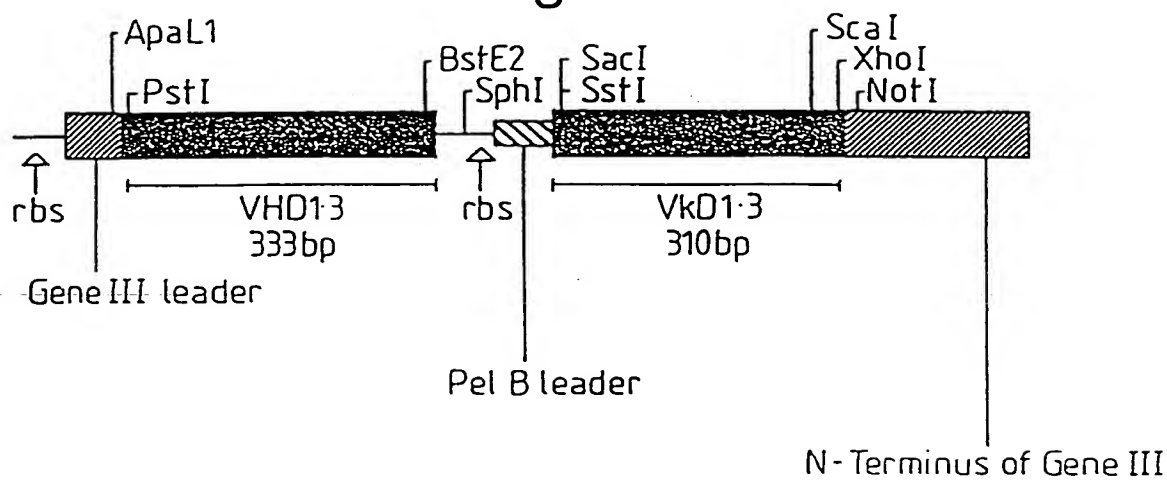


Fig.46.

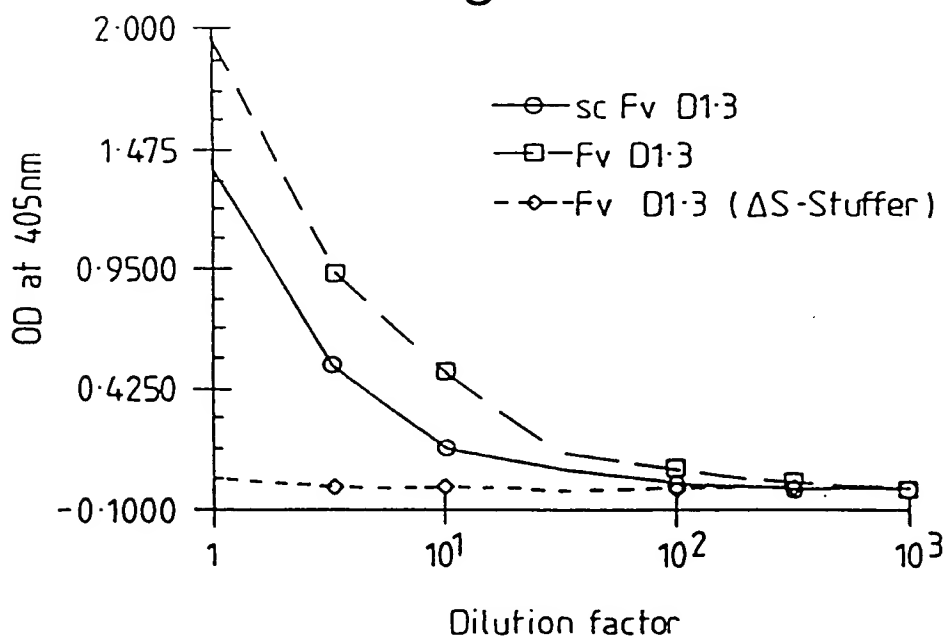


Fig.47.

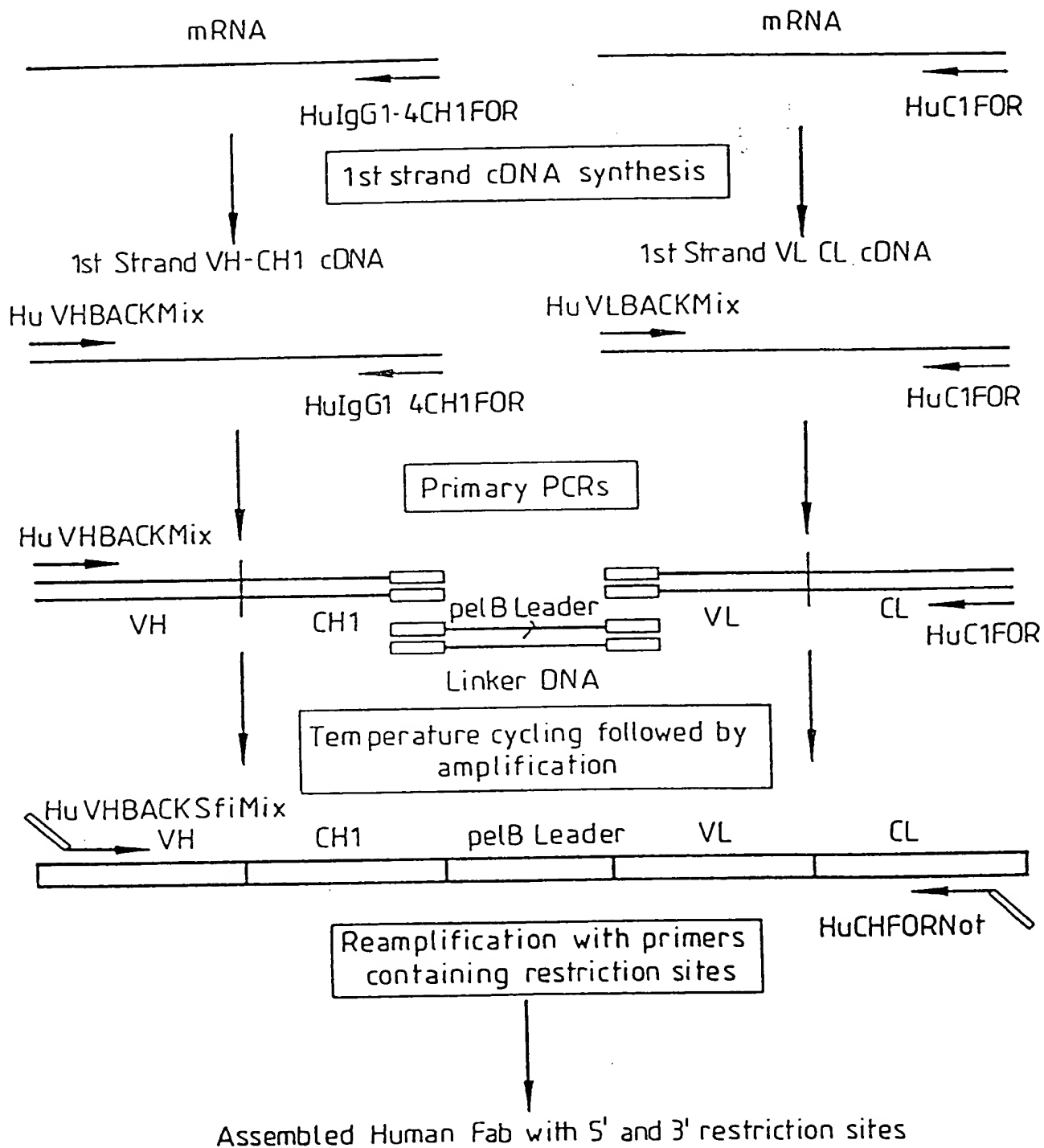


Fig. 48a

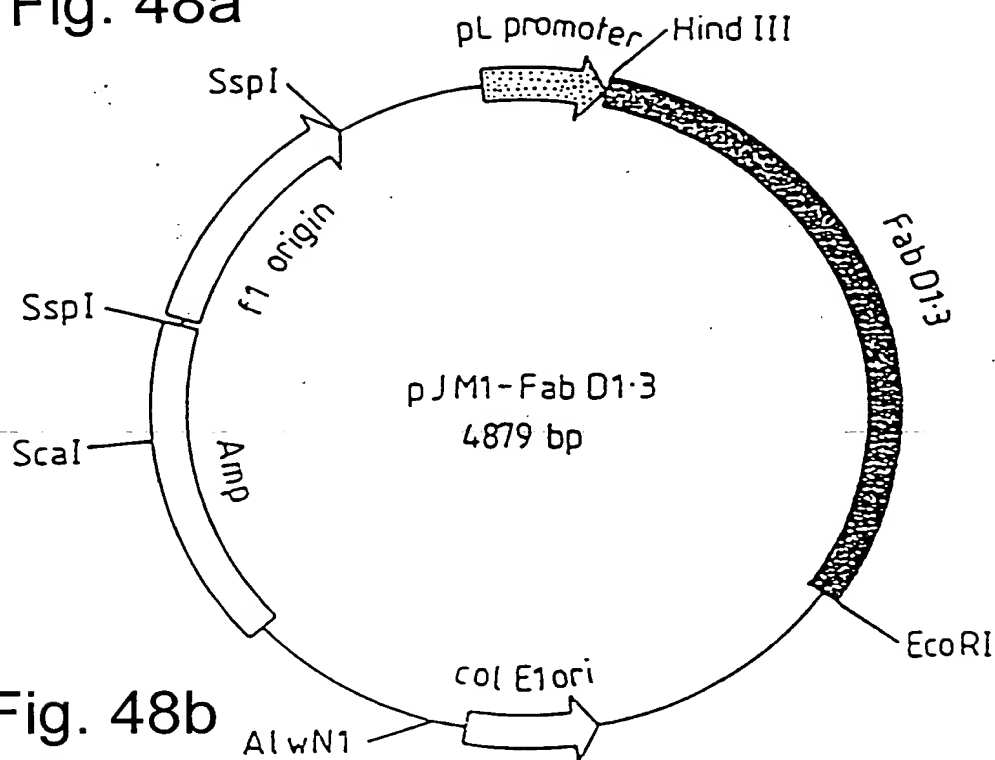


Fig. 48b

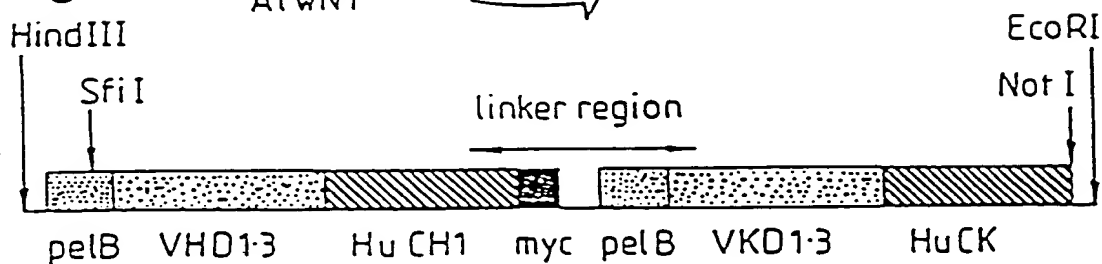


Fig. 48c

← 3' Human CH1 and hinge →  
K P S N T K V D K K V E P K S S T K T H T  
A A C C C C A G C A A C A C C A A G G T C G A C A A G A A G T T G A G C C C A A T C T T C A A C T A A G A C G C A C A C A

→ myc peptide tag →  
S G G E Q K L I S E E D L N \* \*  
T C A G G A G G T G A C A G A G C T C A T C T C A G A G A G A T C T G A A T T A A T A A G G G A G C T T G C A T G C A

(SEQ ID NO. 263)

← pelB leader →  
M K Y L L P T A A A G L  
A A T T C T A T T T C A A G G A G A C A G T C A T A A T G A A T A C C T A T T G C C T A C G G C A G C C G T G G A T T G T

→ 5' Vk →  
L L P A A Q P A M A D I E L T Q S P  
T A T T A C C T G C T G C C A A C C A G C A T G G C G A C A T G A G T T C A C C A G T C T C

(SEQ ID NO. 264)

(SEQ ID NO. 265)

Fig.49.

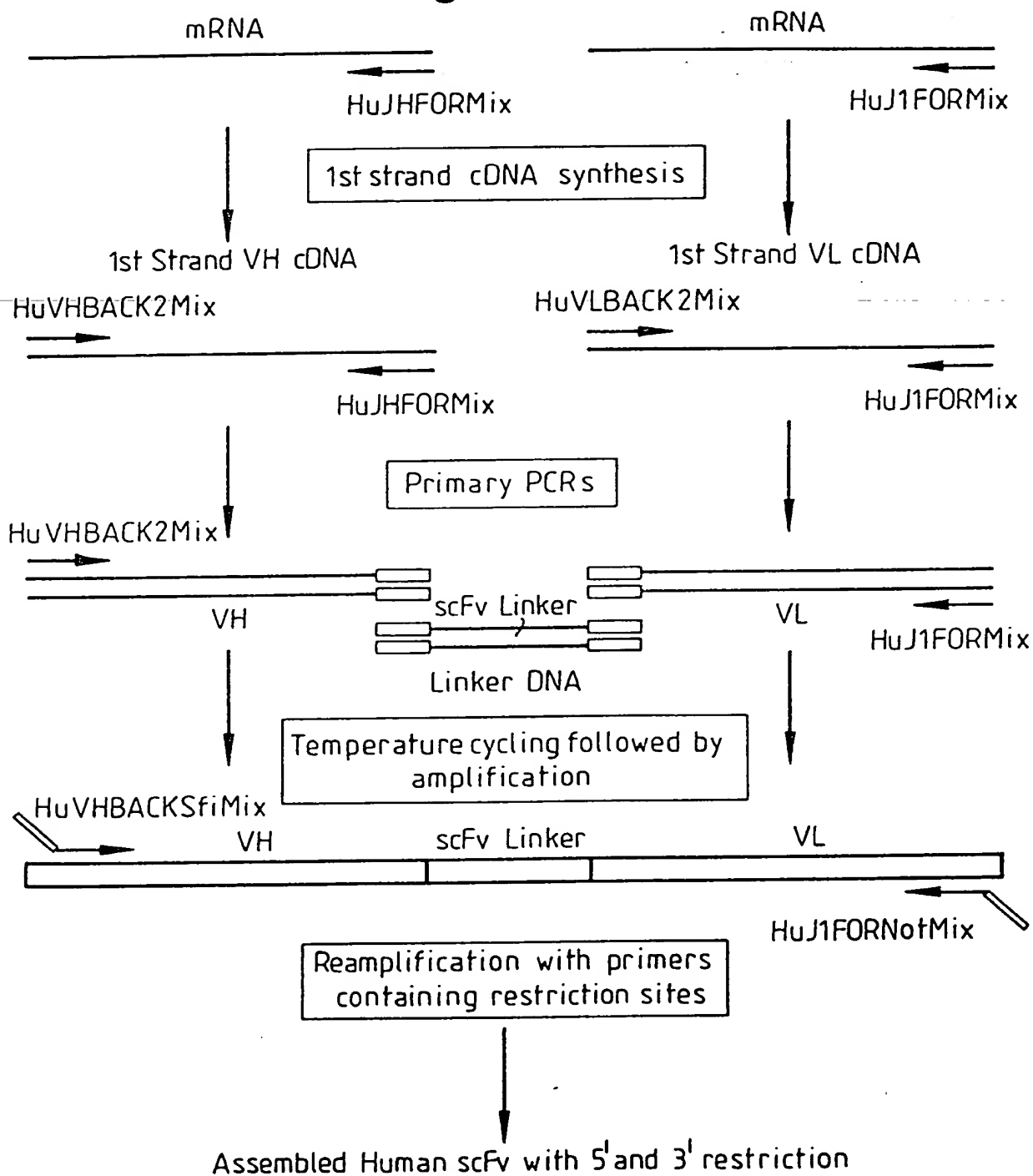


Fig.50a

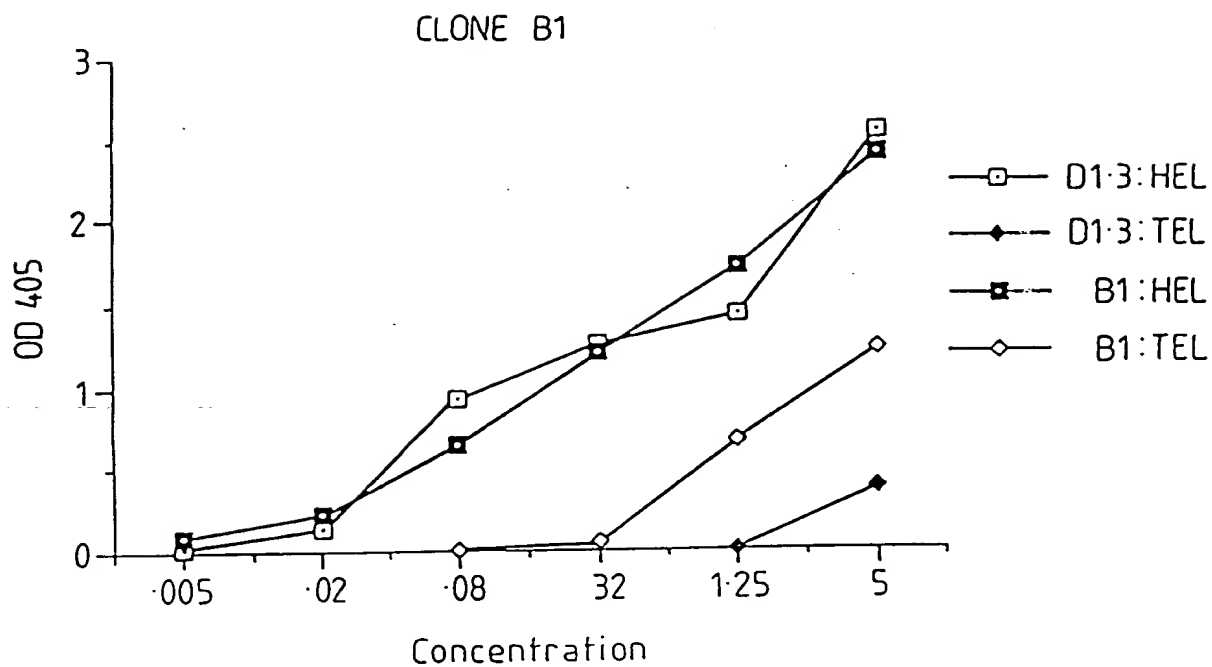


Fig.50b

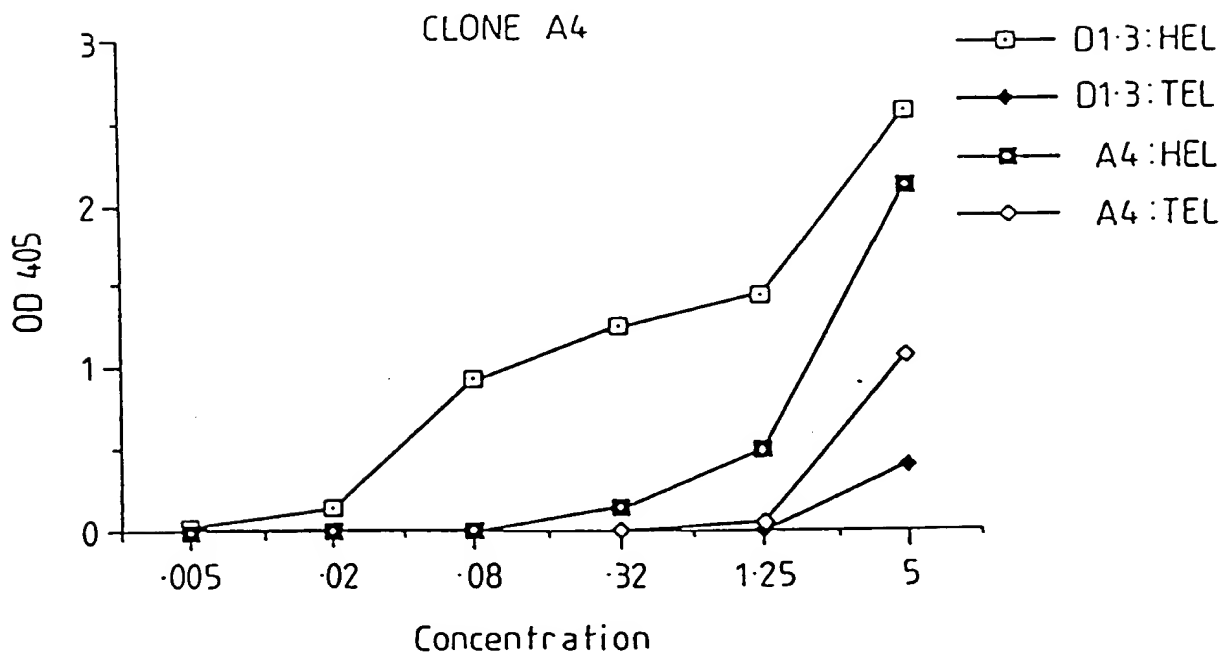


Fig.51.

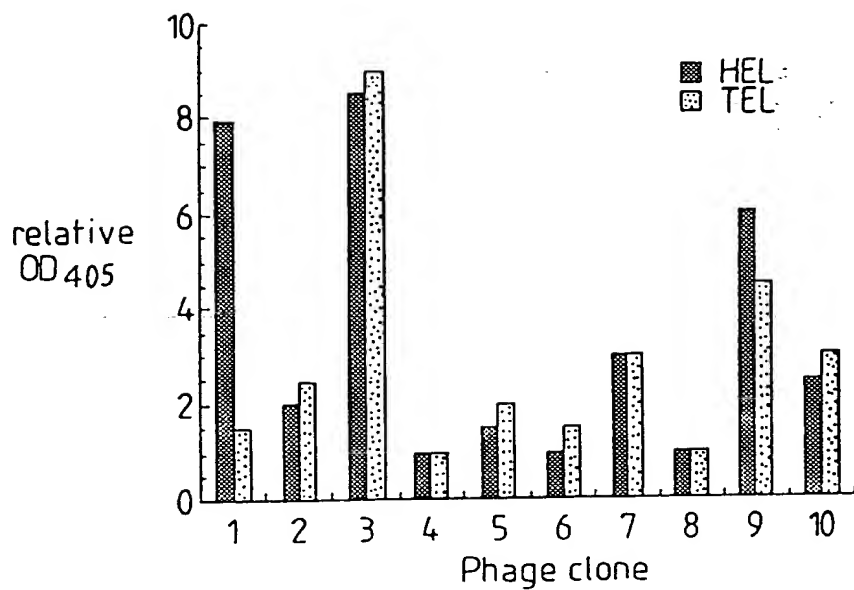


Fig.53.

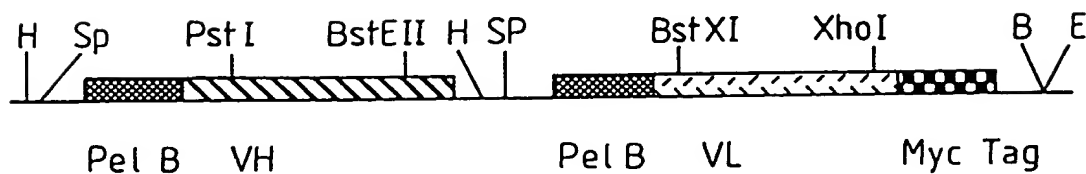




Fig.52.

CDR 1

CDR 2

D1.3 DIQMTQSPASLSASVGETVTITCRASGNIHNYLA WYQQKQKSPQLLVYYTTTLAD  
M1F DIELTQSPSSLSASLGERVSLTCRASQDIGSSLN WLQQEPDGTIKRLIYATSSLDS  
M21 DIELTQSPALMAASPGEKVTITCSVSSSISSNLHWYQQKSETSPKPWIYGTSNLAS

CDR 3

D1.3 GVPSRFGSGGTQYSLKINSLQPEDFGSYQCQHFWSPTPTFGGGTKLEIKR  
M1F GVPKRFGSRGSDYSLTISSESEDFVDYYCLQYASSPWTFGGGTKLELKR  
M21 GVPVRFSGSGGTSYSLTISSEAEADAATYYCQQWSSYPLTFGAGTKLEIKR